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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: April 5, 2003, 10:09:13 ; Search time 6821 Seconds
(without alignments)
9941.290 Million cell updates/sec
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Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenBmbl:\*

1: gb\_ba:\*
2: gb\_htg:\*
3: gb\_ln:\*
4: gb\_om:\*
5: gb\_pat:\*
6: gb\_pat:\*
7: gb\_ph:\*
10: gb\_ro:\*
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11: gb\_ro:\*
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12: gb\_ro:\*
13: gb\_un:\*
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15: em\_ba:\*
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33: em\_htg\_ohu:\*
34: em\_htg\_ovt:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	AB0218	AY04024	BD01281	ABUS181/ 3 BD008348	#790009 100000		AB03849	BD01281	AB05181	BD0082		AY02841	AF 10032	AF05619	AB03398	BD01280	BD0082	AF49058	AF37035	AP004274	LES3066	BDOLZBI	23 BD008251	AY04024	AF49058	AX45965	AF51563		AF2/36/1					Ø	AL7727	AF49782	•	AB03399	AB05506	APOUSS	APUU35U	OHIELDER OF THE
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## ALIGNMENTS

2313 bp mRNA linear PLN 21-MAR-2002	Oryza sativa (japonica cultivar-group) OsNHX1 mRNA, complete cds. AB021878			Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) cDNA . to mRNA.	1ltivar-group)	Streptophyta; Embryophyta; Tracheophyta;	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	)ryza.	
AB021878		AB021878.1 GI:5731736		Oryza sativa (japonica cu		Eukaryota; Viridiplantae	Spermatophyta; Magnoliopl	Ehrhartoideae; Oryzeae; Oryza.	7
RESULT 1 AB021878 LOCUS	DEFINITION ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM				REFERENCE

REFERENCE 1 AUTHORS Fukuda, A., Nakamura, A. and Tanaka, Y.

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Fukuda, A.; Tanaka, Y. and Nakamura, A.
Fukuda, A.; Tanaka, Y. and Nakamura, A.
Submitted (25-DEC-1998) Atsunori Fukuda, National Institute of
Agrobiological Resources, Department of Plant Physiology; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:fukuda@abr.affrc.go.jp, Tel:81-298-38-8376,
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KOFFRNEMT TLFGGAVGTMISFTISTAAIAIFSRMNIGTLDVGDFFPTALLIGENFEVK
KOFFRNEMT TLFGGAVGTMISFTISTAAIAIFSRMNIGTLDVGDFFPLAGAFSTDS
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Molecular cloning and expression of the Na+/H+ exchanger gene in
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Biochim. Biophys. Acta 1446 (1-2), 149-155 (1999)
99326147
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/db_xref="taxon:39947"
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KKQFFRNFATIILFGAAGTLISFVIITFGAMGLFSKLDVGPLEGDYLLAGAIFSATD
SVCTLQVLNQDEAPLIYSLVGEGVNNDATSVVLFWIQNIDINHPDVFVLLQFIGKT
LYLFFGSTVLGYNAGALLSAYIIKKLCFARHSTDREVAIMILMAYLSYMLSMLLDLSGI
LTVFFCGIVMSHYTWHNVTESSRVTKHTFATLSFTARIFLFLVGMDALDIDKWKLA
SSSPKRFIALSAVIIGHTAVGRAAFVPRPLSFLSNLSKESHPKISFNQQVIIWMAGLM
RQAVSIALLASAVIIGHTAVRVNAMITSTIIVVLFSTRWFGLIFRFLYRPLINLLIPPRE
GTAADLSSQSFLDPLTASLLGSDFDVGQLTQVNLQYLLTMPTRSVHRVWRKFDDKFM
RPMFGGRGFVPFVPGSPIERSVHGPGLLGTVTEABDSS"
              Wang, Z., Zhang, J. and Chen, S.
Direct Submission
Submitted (14-JUN-2001) Institute of Genetics, Chinese Academy of Sciences, Datun Road 3, Beljing 100101, China
Location/Qualifiers
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'organism="Triticum aestivum"
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/protein_id="AAK76737.1"
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Triticum aestivum Na+/H+ antiporter (NHX1) mRNA, complete cds.
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1 (bases 1 to 2017)
Wang, Z., Zhang, J. and Chen, S.
Isolation and characterization of two Na+/H+ antiport genes from
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PAT 02-AUG-2002

BD012814 2423 bp DNA linear PAT 02-A Gene coding for protein having an activity to control pH in vacuoles.

GI:22093003

BD012814 BD012814.1

ACCESSION VERSION

LOCUS

BD012814 RESULT 3

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WO 0114560-A/13.

Petunia x hybrida.
Petunia x hybrida.
Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Peprmatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
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SUNTORY LTD, SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI
SUNTORY LTD, SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI
DN WO 011450-A/13
DD 01-MAR-2001
PF 24-AUG-2000 WO 2000JP005722
PR 24-AUG-1999 JP 99P 236800
PR SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI PC
C12N15/29, CO7K14/415, C12N5/10, A0145/00, C12P21/02 CC
SEQUENCE Of DNA coding for protein having an activity to
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Gene coding for protein having an activity to control pH
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llarity 69.9%; Pred. No. 1.8e-164;
Conservative 0; Mismatches 461;
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/db_xxef="taxon:4102"
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Petunia x hybrida cDNA to mRNA. Petunia x hybrida Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Petunia.

Lida,S., Kusumi,T., Yonekura-Sakakibara,K. and Tanaka,Y.
Plant Na-H antiportor

Unpublished

JOURNAL REFERENCE AUTHORS REFERENCE

TITLE

AUTHORS TITLE JOURNAL

FEATURES

(sites)

ORGANISM

Tanaka, Y., Yonekura-Sakakibara, K., Kusumi, T. and Iida, S.
Tanaka, Y., Yonekura-Sakakibara, K., Kusumi, T. and Iida, S.
Direct Submission
Submitted (27-NOV-2000) Yoshikazu Tanaka, Suntory Ltd., Institute
for Fundamental Research; Wakayama-dai, 1-1-1, Mishima, Shimamoto,
Osaka 618 8-8503, Japan (B-mail:Yoshikazu\_Tanaka@suntory.co.jp,
Tel:81-75-962-8807, Fax:81-75-962-8262)

/organism="Petunia x hybrida" /db\_xref="taxon:4102" /note="synonym:Petunia hybrida"

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352. .1974 /gene="PhPurple" gene="PhPurple"

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"Gene coding for protein having an activity to control pH in vacuoles";
Parent number JP03975549-T/13, 23-PEB-2001.
SUNTORY LID, SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI.
                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; Asteridae;
euasterids I; Solanales; Solanaceae; Petunia,
GCGACCGATGTTTGGCGGGGGGGGTTCGTGCCCTTCTCCCCTGGATCACCAACCGAGC 1884
                         1893 GCGTCCAGTTTTCGGTGGACGAGGTTTTGTACCTTTTTGCTCCAGGATCACCGACAGACC 1951
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JP 03075543-T/13

23-FEB-2001

24-AUG-2000 JP 2000005722

24-AUG-1999 JP 99P 236800

SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI

C12N15/29, C07KL4/415, C12NS/10, A01H5/00, C12P21/02
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(Rel. 70, Last updated, Version 1)
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633 TITTAARGCTGGGTTCCAGGTGAAAAAGAAATCGTTCTCCGCAATTTCAGCACTATCAT
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C12N15/09, A01H5/00, C07K14/415, C12Q1/68//C12N5/10, C12N15/00,
                                                                                                 CCTCACCAAGCCGACCCACACTGTCCACTACTACTGGCGCAAGTTCGACGACGCGCTGAT 1825
                                                                                                                    1833 CCTITCAACCCCATCTCATACAGTGCATTAFTACTGGAGAAAGTTTGACAATGCATTCAT 1892
                                                               1773 ACAAGACTCAGAAGCTGATCTGGAACGCCATGTACCCCGTCCCCACAGTTTGCGGGATGCT 1832
1713 AATGATCTTTTTGAACCAACGACCCCAAAATCCTTCATTGTGCCACTTCTTGACAGCAC 1772
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/organism='Atliplex gmelini'
Location/Qualifiers
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E63046
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Patent: JP 2000157287-A 1 13-JUN-2000;
PLANTECH RESEARCH INSTITUTE
OS ALLiplax gmellini
PN JP 2000157287-A/1
PD 13-JUN-2000
PF 16-SEP-1999 JP 1999261606
PR MARIKO SHONO, TAKAHIKO HAYAKAWA, AKIR
PC CI2N15/09, A01H5/00, CO7K14/415, C12Q1
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Shono,M., Hayakawa,T. and Tanaka,A.
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	RESULT 7 E63047 LOCUS LOCUS DEFINITION Na+/H+ antiporter protein and ACCESSTON RE3047 VERSION VERSION VERSION UP 2000157287-A/2. SOURCE unidentified. ORGANISM unidentified. unclassified. Unclassified. Na+/H+ antiporter protein and Tank Na+/H+ antiporter protein and Tank Na+/H+ antiporter protein and	AL Patent: PlanyEdy PLANYEGY POS JP PD 13- PR 16- PR PI 16- PR PL 16- PR PL 16- PR PL 16- PR PL 16- PR PL 16- PR PL 16- PR PL 16- PR PL 16- PR PL 16- PR PL 16- PR PL PL PL PL PL PL PL PL PL PL PL PL PL	cation/Qua'. .1668 cganism="w _xref="ta 34.0%;	Best Local Similarity 70.0%; Pred. No Matches 1115; Conservative 0; Misms Oy 339 ACGACTCCGACTACGCGTCGGTGGTGCCACT OS STATE OF T
y 639 TTTGGAGCCGTCGGGACAATGATATCCTTTTTCACAATATCTGTTGCTGCCATTGCAATA 698  349 TTTGGAGCTGTTGGTACATTGGTATCATTCACCATCATCTGCGGAGCGTTGCAATA 408  599 TTCAGCAGAATGAAATTGGAACGCTGGATGTAGCAATTCTTGCAATTGGAGCCTTC 758  409 TTCAGCAGAATTGGAACATTGGAACGTTGGAGATTTTCTTGCAATTGGAGCATC 758  501 TTTAAGAAATTGGAAATTGGAACATTGCAGAGACTATCTTGCAATTGGTGCAATA 468  502 TTTCTGCGACAGATTCTGTCTGCAGTTGCAGATGAACAATGGAACAACCCCTTT 818  503 TTTCTGCGACAGATTCTGTTTGCAGGATGAGAACAATGAGAACACCCCTTT 618  504 TTGTTGCAGATTCTGTTTGCAGGATTTTTTTTTTTTTTT	### PACGCACTACAGAACTTTGATCTTGTCCACATAGATGCGGCTGTCGTTCTGGAAATTCTTG		949 TTCCTATTCTATAGGGTAGGATGCATTGGACATTGGAGATTTGTTAGT  1299 GACAGACTGGCAAATCCATTGGATGCATTGGACATTGCTAGGATTTGTTAGT  1009 GATAGTCCTGGCAAATCCATTGTGGATTGCTAGGATTTGTTAGT  11359 AGAGCTGCTTTTGTTGTTGCTGTTCTTGTTGCTAGGTCTAGGTTGGATTGTTGGATTGTTGGATTGTTGGATTGTTGGATTGTTG	1119   GAAAAATAACCTGGAGAAGTTGTAATATGGTGGGCTGGGCTGATGAGAGGGCT   1478
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Plant Mol. Biol. 46 (1), 35-42 (2001)
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Hayakawa, T., Hamada, A. and Tanaka, A.
Direct Submission
Submitted (17-FEB-2000) Takahiko Hayakawa, Plantech Research
Institute, Research Center; 1000 Kamoshida-cho, Aoba-ku, Yokohama,
Kanagawa 227-0033, Japan (E-mail:pri0012@cc.m-kagaku.co.jp,
Tel:+81-45-963-3520, Fax:+81-45-962-7492)
Location/Qualifiers
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Atriplex gmelini
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                            AB038492 2637 bp mRNA linear PLN 15-AUG-?
Atriplex gmelini AgNHX1 mRNA for Na/H antiporter NhX1, complete
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Hayakawa,T.
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Caryophyllidae, Caryophyllales, Chenopodiaceae, Atriplex.
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/protein_id="BAB11940.1"
/db_xref="GI:9857314"
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/db_xref="taxon:118074"
1. ~2637
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December   December	RESULT 9  BRO12815  LOCUS  BRO12815  BRO12815  BRO12815  Gene coding for protein having an activity to control pH in vacuoles.  Vacuoles.  Vacuoles.  Vacuoles.  Wacuoles.  Wacuoles.  Wacuoles.  Wacuoles.  Wacuoles.  Wacuoles.  Unidentified.  Wacuoles.  REPERBNOE  Unidentified.  Wacuoles it to 2553)  AUTHORS  AUTHORS  It classes 1 to 2553)  AUTHORS  It classes 1 to 2553  It classes 1 to 2553  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It classes 1 to 2553  AUTHORS  It cla
### 115; Conservative 0; Mismatches 436; Indels 42; Gaps 2;  ###################################	### ### ##############################

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 DB 6; Length 2553;
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PLN 29-MAY-2001
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Nierembergia.
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Tanaka, Y., Yonekura-Sakakibara, K., Kusumi, T. and Iida, S.
Direct Submission
Submitted (27-NOV-2000) Yoshikazu Tanaka, Suntory Ltd., Institute
for Fundamental Research; Wakayama-dai, 1-1-1, Mishima, Shimamoto,
Osaka 618-8503, Japan (B-mail:Yoshikazu Tanaka@suntory.co.jp,
Tel:81-75-962-8807, Fax:81-75-962-8262)
Location/Qualifiers
1. 2553
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                                        1596 Aggigadecriridririrecerridrearirericiaecaaericaaeaaaarecidae 1655
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                                                                                                             1716 GITTCIAIGGCCCTTGCTTAIAATCAGTTTACCAGGGGAGGTCATACTCAGTTACGTGCC
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                                                                                       1419 GAAAAAATAACCTGGAGACAGCAAGTTGTAATATGGTGGGCTGGGCTGATGAAGAGGAGCT
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Plant Na-H antiportor
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/db_xref="taxon:144865"
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/translation="MAFDFGTLLGKONNLTTSDHQSVVSVNLFVALICACIVIGHLLE
ENRWNNESITALVIGSCTGVILLLISGGKNSHILVFSEDLFFTYLLPFIFINGFQVK
KKSFFRNFSTIMLFGAVGTLISFIIISAGAIGIFKKMDIGHLEIGDYLAPATD
SVGTLQVLAQUEFPLLYSLVPEGGVNNDATSVVLFNAVOPFDLSHISTGKALQLIGNF
IXLFASSTFLGVAVAGLLSAFIIKKLYFGRHSTDREVAINILMAYLSYMLAELFYLSGI
LTVFFGGIVMSHYTWHNYTSSRVTTKHTFATLSFIALFFIAFIFINGVATINWAGLM
RGAVSMALAYNGFTRGGHTQLRANAIMITSTITVVLFSTVVFGLMTKPLILLLLESQK
HILRMISSEPMTPKGFIYDPLLDSTQDSEADLGRHVPRFPRILKHLLSTFSHTUHTYWRK
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1356 ALCCTCACTGTGTTTTTCTGTGGGATCGTGATGTCTCACTATACCTGGCATAATGTGACT
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                                                                                                                                                                                                                                                33.9%; Score 790; DB 23; Length 2553; 69.7%; Pred. No. 1e-163; Live 0; Mismatches 465; Indels 9
                                                                                                                                                                                                                              BP; 666 A; 487 C; 535 G; 865 T; 0 other;
                                                                  Nierembergia hybrida
19 03075543-T/14
23-F8D-2001
24-AUG-2000 JP 2000005722
24-AUG-1999 JP 99P 236800
SHIGENU IIDA, SACHIKU TANAKA, YOSHISHIGE INAGAKI
C12N15/29, C07K14/415, C12N5/10, A01H5/00, C12P21/02
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/organism="Nierembergia hybrida"
                                                                                                                                       Location/Qualifiers
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Matches 1088; Conservative
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ABUS4979 2173 bp mRNA linear PLN 19-JUN-2001
Ipomoea tricolor ItNHX1 mRNA for Na+/H+ exchanger, complete cds.
ABUS4979
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Direct Submission
Submitted (23-JAN-2001) Sachiko Fukada-Tanaka, National Institute
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for Basic Biology, Division of Gene Expression and Regulation 1;
Myodaiji-cho, Okazaki, Alichi 444-8585, Japan
(E-mail:sachiko@nibb.ac.jp, Tel:81-564-55-7682, Fax:81-564-55-7685)
Location/Qualifiers
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Convolvulaceae, Ipomoea.
                                                                                                                                                                                                  Yamaguchi,T., Fukada-Tanaka,S., Inagaki,Y., Saito,N.,
Yonekura-Sakakibara,K., Tanaka,Y., Kusumi,T. and Iida,S.
Genes encoding the vacuolar Na+/H+ exchanger and flower coloration
Plant Cell Physiol. 42 (5), 451-461 (2001)
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0; Mismatches 459;
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/db_xref="taxon:89664"
1. 72173
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/product="Na+/H+ exchanger"
/protein_id="BAB60901.1"
/db_xref="G1:14488270"
                                                       pomoea tricolor cDNA to mRNA.
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/gene="ItNHX1"
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KKQFFRIFITIMLFGAATLVSCHYGEGVNNDATSYVLFRID IGTLDIGDYLAIGA FRATD
SVCTLQVLNQDDTPLLYSLVFGEGVNNDATSYVLFRID IGTLDIGDYLAIGA FRATD
SVCTLQVLNQDDTPLLYSLVFGEGVNNDATSYVLFRID IGTLDIGDYLAIGA FRATD
LYLFFGFLLGYTGGLLSAYVTKKLYFGRHSTDREVALWYLMAYLSYMLAELFYLSGI
LTVFFCGI VMSHYTWHNYTESSRVTKHTFATLSFVARI FTFLYVGMDALDIEKWRFV
KGSPGTSVAASAMLMGLIMAGRAAFVFPLSFLTINLAKKSPTEKI SIKQQVII WWAGLM
RGAVSMALLAYNGFTRSGHTQLRENAIMITSTITVVLFSTVVFGMTEPLIRLLIPHPK
HTTNHILSDPSTPFSKLSQPLLEEGQQDSYADLVGPTVPRPGSLRALLTTPHTHYWYYW
RKFDDAFMRPVFGGRGFAPFVPGSPTERSVRGGQ"
                                                                                                                                                                                                                                                                                                                     AXU28416 2135 bp mRNA linear PLN 21-JUN-2002
Citrus x paradisi sodium/proton exchanger mRNA, complete cds.
AY028416
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.
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Porat, R., Povancello, D., Ben-Hayyim, G. and Lurie, S.
A heat treatment induced the expression of a Na+/H+ antiport gene (CNHXI) in citrus fruit fruit Plant Sci. 162 (6), 957-963 (2002)
Plant Sci. 162 (6), 957-963 (2002)
Porat, R., Lurie, S. and Povancello, D.
Direct Submission
1813 TTGCGCATGCTGCTAAGGACGCCACCACCGTGCACCGCTACTGGCGTAAGTTTGAC 1872
                                                                                                          1815 GACGCGCTGATGCGACCGATGTTTGGCGGGCGCGGGTTCGTGCCCTTCTCCCCTGGATCA 1874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-0CT-2001) Postharvest Sciences, ARO, The Volcani Center, Bet Dagan 50250, Israel Sequence update by submitter on Oct 1, 2001 this sequence version replaced gi:13508486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-MRR-2001) Postharvest Sciences, ARO, The Volcani Center, Bet Dagan 50250, Israel 3 (Dases 1 to 2135) Porat.'. Lurie, S. and Povancello, D. Direct Submission
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/product="sodium/proton_exchanger"
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Pred. No. 2e-160;
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/db_xref="taxon:37656"
/tissue_type="peel"
/note="heat-induced"
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/db_xref="GI:15812035"
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Best Local Similarity 68.3%;
Matches 1097; Conservative
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Arabidopsis thaliana sodium proton exchanger Nhx1 mRNA, partial
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WMNESITALLIGLGTGVTILLISKGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQ
FFRNFVTIMLFGAVGTIISCTIISLGVTQFFKKLDIGTFDLGDYLAIGAIFAATDSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Arabidopsis thaliana proton transporters, AtNhxl and Avpl, can function in cation detoxification in yeast
Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1480-1485 (1999)
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TCGATTGCTCTTGCTTACAATAAGTTTTACAAGATCTGGCCATACTCAGCTGCACGGCAAT 1541
                                                                                                                            ATGACAAAGCCATTGATCAGGCTGCTGCTACCGGCCTCCAGGCCATCCTGTCACCTCTGAG 1661
                                                                                                                                                                                          CCTTCATCACCAAAGTCCCTGCATTCTCCTCTCCTGACAAGCATGCAAGGTTCTGACCTC 1721
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Gaxiola, R.A., Rao, R., Sherman, A., Grisafi, P., Alper, S.L. and
                    GACTCTTACGCTGACCTTGTTGGCCCTACTGTTCCCCGTCCTGGCAGCTTGCGTGCTCTT
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/codon start=1

/product="sodium proton exchanger Nhx1"

/protein id="AAD16946.1"

/db_xref="G1:4324597"

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/organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db xref="taxon:3702"
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Submitted (12-NOV-1998) Whitehead,
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VSMALAYNKETRAGHTDVRGNAIMITSTITVCLFSTVVFGMLFKPLISYLLPPQNATT
SMLSDDNTPKSIHIPLLLQVDSFIEPSGNHNVPRPDSIRGFLTRFTVHYYWRQFDDS
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Rosidae, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 1617)
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Arabidopsis thaliana Na+/H+ antiporter (NHX1) mRNA, complete cds.
AF510074 GI:21105719
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Back,S.H., Kim,H.S., Lee,Y.T., Lee,M.H. and Yun,S.J.
Direct Submission
Submitted (07-MAY-2002) Rice Research Division, National Honam Agricultural Experiment Station, Songhak-dong, Iksan, Jeonbuk 570-080, Republic of Korea
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                                           927 TGCGGAGACATTTATTTTCTTGTATGTTGGAATGGATGCCTTGGACATTGACAAGTGGAG 986
                TGCTGAGACTTTTCTCTTCCTGTATGTTGGGATGGATTGGATATTGAAAAATGGGA
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PLOULMQDETPLLSSLVFGEGVVUNDATSVVVFNAIQSFDITHLNHEAAFHLGGNFLYL
FLLGTLLGAATGLISAVVIKKLYFGHHSTDREVALMMLAMAYLSYMLABLFDLGSILTV
PFCGIVWSHYTWHNVTESSRITTKHTFATLSFLAFTFIFLYCMDALDIDKWRSVSDT
PGTSIAVSSILMGLWWGRAAFVFDLSFLSNIAKKQQSEKINFNMQVVIWWSGLWRGA
VSMALAYNKFTRAGHTDVRGNAIMITSTITVCLFSTVVFGMLTKPLISYLLPHQNATT
SMLSDDNTPKSIHIPLDQOSFIEPSGNHNVPRPDSIRGFLTRPTRTVHYYWRQFDDS
FMRPVFGGRGFVPFVPGSPTERNPPDLSKA"
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|db xref="G1:21105720"
|translation="MLDSLVSKLPSLSTSDHASVVALNLFVALLCACIVLGHLLEENR
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                                                /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
                                                                                                                                                                                                                 /codon_start=1
/product="Na+/H+ antiporter"
Location/Qualifiers
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Matches 1077; Conservative
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                                             687 CGGTCTGATAAGTGCGTATGTTATCAAGAAGCTATACTTTGGAAGGCACTCAACTGACCG
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Search completed: April 5, 2003, 14:52:29 Job time : 6834 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

April 5, 2003, 10:03:13; Search time 541 Seconds (without alignments) 9698.995 Million cell updates/sec Run on:

Title: Perfect score:

Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4370478 Total number of hits satisfying chosen parameters: 2185239 segs, 1125999159 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

seq_101002:* DS2/gcgdata/geneseq/geneseqn-embl/NA1980 DS2/gcgdata/geneseq/geneseqn-embl/NA1981 DS2/gcgdata/geneseq/geneseqn-embl/NA1981 DS2/gcgdata/geneseq/geneseqn-embl/NA1981 DS2/gcgdata/geneseq/geneseqn-embl/NA1981 DS2/gcgdata/geneseq/geneseqn-embl/NA1986 DS2/gcgdata/geneseq/geneseqn-embl/NA1986 DS2/gcgdata/geneseq/geneseqn-embl/NA1986 DS2/gcgdata/geneseqg/geneseqn-embl/NA1987 DS2/gcgdata/geneseq/geneseqn-embl/NA1987 DS2/gcgdata/geneseq/geneseqn-embl/NA1987 DS2/gcgdata/geneseq/geneseqn-embl/NA1987 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA1997 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/geneseqn-embl/NA2007 DS2/gcgdata/geneseq/genesequ-embl/NA2007 DS2/gcgdata/geneseq/genesequ-embl/NA2007 DS2/gcgdata/geneseq/geneseq-embl/NA2007 DS2/gcgdata/geneseq/geneseq-embl/NA2007 DS2/gcgdata/geneseq/genes	/SIDS2/gcgdata/geneseq/geneseqn-embl/NA198.DA /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DA /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DA /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DA /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.Da /SIDS2/gcgdata/geneseqn/geneseqn-embl/NA1980.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001.Da /SIDS2/gcgdata/geneseqn-embl/NA2001.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001.Da /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001.Da
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	cDNA encoding rice	Gene regulating th	Atliplex gmelini N	Gene regulating th	Arabidopsis thalia	Gene regulating th	Arabidopsis thalia	Gene regulating th	. Arabidopsis thalia
ID	;		AAA72926						AAZ22592
DB	21	22	21	22	20	22	20	22	20
% Query Match Length DB	2330	2423	1668	2553	2178	2237	2284	2361	1788
% Query Match	100.0	34.1	34.0	33.9	33.0	33.0	32.1	30.5	21.8
Score	2330	793.4	791.4	790	768.8	768.8	746.8	711.8	508.8

Result No.

Fukuda A, Tanaka Y;

DNA encoding Physc Rice Na/H antiport Arabidopsis Na/H a Corn tassel-derive Cat flea HMT Na/H Cat flea HMT Na/H Cat flea HMT Na/H Cat flea HMT Na/H Rice Na/H antiport Drosophila melanog Human transporter Arabidopsis thalia Human secreted pro Human secreted pro Drosophila melanog Colo Brosophila melanog Colo adenocarcino CDNA sequence #118 Human Secreted pro Drosophila melanog Colo adenocarcino CDNA sequence #118 Human secreted pro Drosophila melanog Colo adenocarcino CDNA sequence #118 Human secreted pro Drosophila melanog Human transporter Arabidopsis thalia Arabidopsis thalia Human secreted exp Human secreted exp Human secreted exp Human secreted opponing novel Drosophila melanog Human secreted exp Human secreted exp Human secreted pro DNA encoding novel	Kaposi's sarcoma-a Nucleotide sequenc Kaposi's sarcoma-a KSHV LUR DNA (nucl KSHV long unique c
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## ALIGNMENTS

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OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance; ss.
                                                                                                                                               Location/Qualifiers
297..1904
/*ttea
/product= "Rice Na+/H+ antiporter"
                                                                              CDNA encoding rice Na+/H+ antiporter, OsNHX1.
                                                                                                                                                                                                                                                                              (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
                    AAA61876 standard; cDNA; 2330 BP.
                                                                                                                                                                                                                                                            98JP-0365604.
                                                                                                                                                                                                                                         99WO-JP07224.
                                                          07-NOV-2000 (first entry)
                                                                                                                                                                                                  WO200037644-A1
                                                                                                                              Oryza sativa.
                                                                                                                                                                                                                                                            22-DEC-1998;
                                                                                                                                                                                                                                         22-DEC-1999;
                                                                                                                                                                                                                    29-JUN-2000
                                        AAA61876;
RESULT 1
AAA61876
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DNA encoding a sodium ion and proton counter-transporter protein of rice origin for production of salt tolerant rice transformants -
                                                     Claim 1b; Fig 1; 43pp; Japanese.
WPI; 2000-442672/38.
P-PSDB; AAB11832.
```

This sequence represents cDNA encoding a rice Na+/H+ antiporter (countertransporter), OSNHX1. The invention relates to OSNHX1 and nucleic acids which encode it; vectors, host cells and transgenic plants containing OSNHX1 nucleic acids, recombinant expression of OSNHX1; and antibodies which recognise OSNHX1. OSNHX1 nucleic acids are useful in the production of salt tolerant transgenic plants.

Sequence 1310 BP; 560 A; 538 C; 569 G; 663 T; 0 other;		Gaps 0;	F 60	3 120   3 120	3 180 - 3 180	24 0 42 0 42 0 44 0	300	360 360 41-44	2 420 2 420	4 80 4 80	540     540	4 600 4 600	4 660 4 660	A 720 A 720	r 780
Sequence 2330 BP; 560 A; 538 C; 569 G; 663 T;  Lesty Match  set Local Similarity  100.0%; Score 2330; DB  set Local Similarity  100.0%; Pred. No. 0;  RICHERS 2330; Conservative  0; Mismatches  1 GAGAAGAGATTTTGTAGCGAGCTCGCGCGAATGCGAAGC  61 ACCAANTCCCGATTTGTAGCGAGCTCGCGCGAATGCGAAGC  61 ACCAANTCCCGATTTGTAGCGAGCTCGCCGCCACGT	0 other; 21; Length	Indels 0;	Caaccgagagaggtctcga 	TCCTCGTTTCAATCTGTTC                 TCCTCGTTTCAATCTGTTC	CCGGGAATTGTCGAATTAG                 CCGGGAATTGTCGAATTAG	AAGCTCCGCATCTTGCGGC 	TCGCCGCCGGTGAGGCATG                TCGCCGCCGGTGAGGCATG	GACCTCCGACTACGCGTCG 	CATCGTCCTCGGCCACCTC	CATCATCGGGCTCTGCACC	CTTATTCGTCTTCAGTGAG 	TGCAGGTTTTCAGGTAAAG.                TGCAGGTTTTCAGGTAAAG.	TGGAGCCGTCGGGACAATG               TGGAGCCGTCGGGACAATG	CAGCAGAATGAACATTGGA 	TTCTGCGACAGATTCTGTC
Sequence 2330 BP; 560 A; 5:  Leary Match  set Local Similarity 100.03  atches 2330; Conservative  1 GAGAAGAGATTTTGTAGGAGA  61 ACCAAATCCCGATTTCTAACGAATCAACGAATCCTAACGAATCCTAACGAATCTTTGTT  121 TCTGCGAATCGAATTCTTTGTT  121 TCTGCGAATCGAATTCTTTGTT  181 CATTCACCAACGAGCAAGAGGGAGGAATCTTTGTT  181 CATTCACCAACGAGCAAGAGGGAGGGCAATCATCTTGTT  181 CATTCACCAACGAGCAAGAGGGAGGGAATCGAACGAGGAGGAATCGAATCTTTGTT  181 CATTCACCAACGAGCAAGAGGGAGGGAGGAATCTTCTTGTT  241 GAAATCTCCTTCTTCTTCTTGTT  301 GGATGGAGAATCGTTGTTCTTGTT  481 GCGTGGTAATCTTGCTGATGAA  481 GCGTGGTAATCTTGCTGATGAA  481 GCGTGGTAATCTTCCTGATGAA  481 GCGTGGTAATCTTCCTGATGAACGTTAACTTAACTTCTTCGAATTTTCCGGAATTTTCGAATTTTCCGGAATTTTCGAATTTTCCGGAATTTTCGTAATTTTTCCGGAATTTTTCCTAATTTTTTTT	C; 569 G; 663 Score 2330;	8; Fred. No. U; O; Mismatches	actcgcggaatgcgaagc 	CTGAATCCCCCCCCCACGT 	ITTTTTTCTCTAATTTTA 	3GAGTGGATTGGTTGGTTA                  3GAGTGGATTGGTTA	CGGTGGCTGGCCGGAGAAG 	GCTGGGGCTCTGTACAC	rcgcgcrgcrcrgcgccrg 	ATGAGTCCATCACCGCGCT 	ccaaagggaagagctcgca 	rcctccgarcarctrcaa 	rcatgacgatcacattatt 	rtgctgccattgcaatatr                 rtgctgccattgcaatatr	TTGCAATTGGAGCCATCTT
Sequence Seq	2330 BP; 560 A; 100.	1 Similarity 100.0330; Conservative	agaagagagttttgtagcga( 	ccaaatcccgatttctcaac 	TGCGAATCGAATTCTTTGT 	attcaccaacgagcaagagg                attcaccaacgagcaagagg	VATCTCGCTCTCTTCTCTG( 	AATGGAGGTGGCGGCGCCCC 	GGTCCATCAACCTGTTCG	CGAGGAGATCGCTGGGTCA 	CGTGGTCTTGCTGATGA( 	ICTCTTCATCTACCTCC	aagcaaticticcggaati 	ATCCTTTTCACAATATCTA: 	SCTGGATGTAGGAGATTTTC
	Sequen	atches 2.													

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Sequence 2423 BP; 621 A; 428 C; 518 G; 856 T; 0 other;

in horticulture.

SXS

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The present sequence is a gene, which encodes a protein with vacuolar pH regulatory activities. The gene enables flower colour to be controlled via regulation of the vacuolar pH, colours can range from blue to red in colour spectrum. The gene is useful in controlling flower colour to give new breeds of colourful plants for cut flowers, particularly applicable
                                                                                                                        2040
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                                                                    1980
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1861 TCTCCCCTGGATCACCAACCGAGCGAGAGCCATGGAGGAGAAGATGAACAGTGCAAAGAAATG
                                                                                                                                                                                                                                                                                                                    GTTGGCGGGTGTTCTTTCCTAGTTGCCACCTGCATGTAAATGAAATTCTCCGCCAAAA
                                          2041 CAGAACTTCAGATGGTGCCTCACCAAGGCCTAAGAGCCCAGGAGGACCTTCTGATAATGGT
                                                                                                                                                                                                                                     TCCGACAACCTGTAAATTTTGTAGATTAACAGCCCCCATTTGTACCTGTCTATA
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                                                          1981 AGTTTTGGGTTTGTAGAGTTTGGCTGCTAATGAGTTGTTGATAGTGCCTATATTCTT
                                                                                                                                                     CAGAACTTCAGATGCTCCTCACCAAGGCCTAAGAGCCAGGAGGACCTTCTGATAATGGT
                                                                                                                                                                                                        AGTITITGGGTTTTGGGTTTTGGCTGCTAATGAGTTGTTGATAGTGCCTATATTCTT
                                                                                                                                                                                                                                                                                                                                                                                       Vacuole pH regulation; flower colour; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene regulating the pH of vacuoles
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present sequence encodes an Na+ and H+ antiporter protein isolated
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               from Atliplex gmelini. The Na+ and H+ antiporter protein and gene encoding it are useful for the preparation of transformed plants with high salt tolerance, e.g. for growth in arid land.
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                                                                                                                   Length 1668;
                                                                                                                                                  42;
                                                                                                               34.0%; Score 791.4; DB 21; Length
70.0%; Pred. No. 2.9e-208;
.ive 0; Mismatches 436; Indels
                                                                                  Sequence 1668 BP; 397 A; 342 C; 376 G; 553 T; 0 other;
                                                                                                               Query Match
Best Local Similarity 70.0°
Matches 1115; Conservative
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949 TICCTATITCTATATGTCGGTATGGATGCATTGGACATTGAGAAGTGGAGATTTGTTAGT 1008
                                                                                                                                                                                                     GTGTCGATTGCTCTTGCTTACAATAAGTTTACAAGATCTGGCCATACTCAGCTGCACGGC 1538
                                                                                                                                                                                                                                                                                                                                                                             CAAGATTATGAAGTTGATGTGGGAAACGGAAACCATGAAGACACCACTGAGCCGCGGACT 1488
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                                                                                                               1069 AGAGCAGCTTTTGTTTTCCCCTTATCCTGGTTGATGAACTTTGCCAAGAAATCGCAAGT
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                                                      GATAGTCCTGGCATTTCTGTTGCTGTGAGTTCCATATTGCTAGGTCTAGTCATGGTTGGA
                                                                                                                                            GAAAAAATAACCTGGAGACAGCAGTTGTAATATGGTGGGCTGGGCTGATGAGAGGAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene regulating the pH of vacuoles
                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGGTTCTGACCTCGAGAGTACAACC--
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                                                 Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable in horticulture
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                                                                                                                                                                                                                                                                                                                                                  Length 2553;
                                                                                                                                                                                                                                                                                                                                              Query Match 33.9%; Score 790; DB 22; Length 2
Best Local Similarity 69.7%; Pred. No. 9.1e-208;
Matches 1088; Conservative 0; Mismatches 465; Indels
                                                                                                                                                                                                                                                                                                               Sequence 2553 BP; 666 A; 487 C; 535 G; 865 T; 0 other;
                                                                                                                                              Example 7; Page 45-49; 68pp; Japanese
WPI; 2001-191648/19.
               P-PSDB; AAB73253
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1296 ATAATGATACTCATGGCGTACCTATCATACATGCTTGCTGAATTATTCTATTTAAGTGGA 1355
                                                                                                                      1179 GAGAGTICAAGAGTIACAACAAAGCACGCATTIGCAACTCTGTCCTTCATTGCTGAGACT 1238
                                                                                                                                                                                                       TITCTCTTCCTGTATGTTGGGATGGATTGGATATTGAAAAATGGGAGTTTGCCAGT 1298
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                                        1119 ATTCTCACCGTATTCTTCTGTGGTATTGTAATGTCACTTACACTTGGCATAACGTCACA
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The invention relates to an isolated nucleic acid molecule encoding a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and capable of increasing salt tolerance in a cell. This sequence corresponds to the gene encoding the AtNHX1 transporter from Arabidopsis thaliana.

The Na/H transporter polypeptides provide a means of intracellular salt ananagement, particularly in plants. The sequences are useful for producing transgenic plants that are capable of surviving in soil with high salt levels that would normally inhibit growth of the crop species. This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and poor irrigation, e.g. in India, Australia, and prairies in USA or Canada. Commercial strawberries, spinach, lettuce, irice, soybean, corn, wheat, rye, barley, atriplex, sorghum, alfalfa, salicornia and others would benefit from increased salt tolerance.
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                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules encoding sodium/proton transport polypeptides, useful in genetic engineering salt tolerance in crop plants
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Pred. No. 6.1e-202;
0; Mismatches 487; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2178 BP; 576 A; 413 C; 472 G; 717 T; 0 other;
                                                                                                                                                                                                                                                                                         Snedden W, Aharon G;
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68.6%;
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Arabidopsis thaliana
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Best Local Similarity
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                                                                                                                                                                                                  BLUMWALD E.
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689 CATTGCAATATTCAGCAGAATGAACATTGGAACGCTGGATGTAGGAGATTTTCTTGCAAT 748

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Sodium; proton; antiport; transporter; salt tolerance; salt management; transgenic plant; survival; soil; farming; accumulation; irrigation;

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                                                                          TGGTGCCATATTTGCTGCAACAGATTCAGTATGTACACTGCAGGTTCTGAATCAAGACGA
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The present sequence is a gene from Morning Glory, which encodes a protein with vacuolar pH regulatory activities. The gene enables flower colour to be controlled via regulation of the vacuolar pH, colours can range from blue to read in colour spectrum. The gene is useful in controlling flower colour to give new breeds of colourful plants for cut flowers, particularly applicable in horticulture.
                                                     1752 CTTCTTGACACGGCCCACTCGAACCGTGCATTACTACTGGAGACAATTTGATGACTCCTT 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGTGGTAGAAAAAGGGGAAGAACAAAAATGGCGTTCGGGTTGTCTTCTTTGCTCCAAAA 331
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                                 1823 GATGCGACCGATGTTTGGCGGGGGGGTTCGTGCCCTTCTCCCCCTGGATCACCGAACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 33.0%; Score 768.8; DB 22; Length 2237; Best Local Similarity 67.9%; Pred. No. 6.2e-202; Matches 1130; Conservative 0; Mismatches 507; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                   Vacuole pH regulation; morning glory; flower colour; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 26-30; 68pp; Japanese.
                                                                                                                                                                                                                                                                                                                                    Gene regulating the pH of vacuoles
                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                               AAF75752 standard; DNA; 2237
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                                                                                                      1883 GCAGAGCCAT 1892
                                                                                                                                         1872 GAGAAACCCT 1881
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P-PSDB; AAB73251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200114560-A1
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449 CATCACCGCGCTCATCATCGGGCTCTGCACCGGCGTGGTGATCTTGCTGATGACCAAAGG 508

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	CCTCCTCCTCC 568	GAATTTCATGAC 628            GAACTTCATGAC 631	ATCTATTGCTGC 688             ATCATTTGGTGC 691	TTTTCTTGCAAT 748                  TTATTTAGCAAT 751	CAATCAGGATGA 808                   CAGTCAGGATGA 811	TGCTACATCAAT 868              TGCTACATCTGT 871	GGCTGTCGTTCT 928 	TGGAGTATTTGC 988       GGGGGAGAAT 991		TGAGTTGCTAGA 1108            CGAGTTATTCTA 1111	TTACACTTGGCA 1168                 TTATACCTGGCA 1171	TCTGTCCTTCAT 1228            TCTGTCATTTGT 1231	TGAAAATGGGA 1288               CGAGAATGGAA 1291	GCTAGGATTGGT 1348               GGTAGGCCTAAT 1351	CCTAACAAAAA 1408                     CTTAGCAAAGAA 1411	GGCTGGGCTGAT 1468              GGCTGGCCTAAT 1471	TGGCCATACTCA 1528                GGGGCATACGTC 1531	TTTTAGCACTAT 1588
	GAAGACTCGCACTTATTCGTCTTCAGTGAGGATCTCTTCTTCATCTACCTCCTCCCTC	GATCATCTTCAATGCAGGTTTTCAGGTAAAGAAAAGCAATTCTTCCGGAATTTCATGAC 	GATCACATTATTIGGAGCCGICGGGACAAIGAIATCCTITITCACAAIAICTATTGCIGC 	CATTGCAATATTCAGCAGAATGAACATTGGAACGCTGGATGTAGGAGATTTTCTTGCAAT 	tggagccatctttttctgcgacagattctgtctgcacattgcaggtcctcaatcaggatga 	GACACCCTTTTTGTACAGTCTGGTATTCGGTGAAGGTGTTGTGAACGATGCTACATCAAT 	TGTGCTTTTTCAACGCACTACAAACTTTGATCTTGTCCACATAGATGCGGCTGTCGTTCT 	GAAATICTIGGGGAACTICTITIATTIATITITGCGAGCACCTICCTIGGAGIATITGC 	TGGATTGCTCAGTGCATACATAATCAAGAAGCTATACATTGGAAGGCATTCTACTGACCG 	TGAGGTTGCCCTTATGATGCTCATGGCTTACCTTTCATATATGCTGGCTG	tttgagcggcattctcaccgfattcttctgrggfattgfaatgtcacattacacttggca 	taacgtcacagagagttcaagagttacaacaaggacgcatttgcaactctgtccttcat 	TGCTGAGACTTTTCTTCCTGTATGTTGGGATGGATGCATTGGATATTGAAAAATGGGA 	GTTTGCCAGTGACAGACCTGGCAAATCCATTGGGATAAGCTCAATTTTGCTAGGATTGGT 	TCTGATTGGAAGAGCTGCTTTTGTATTCCCGCTGTCGTTCTTGTCGAACCTAACAAGAA 	ggcaccgaatgaaaaataacctggagacagcaagttgtaatatggtgggctgggctgat 	GAGAGGAGCIGIGICGATIGCICTIGCITACAATAAGITTACAAGAICIGGCCATACTCA 	GCTGCACGGCAATGCAATAATGATCACCAGCACCATCACTGTCGTTCTTTTAGGACTAT
 452 CATT	509 GAAGA      512 AAAGA	569 GATCA      572 TATAA	629 GATCA      632 AATTA	689 CATTC   692 GGTCA	749 TGGAC       752 TGGTC	809 GACAC       812 GACGC	869 TGTGC      872 GGTCC	929 GAAAT 	989 TGGAT      992 TGGAC	1049 TGAGG       1052 TGAGG	1109 TTTGP	1169 TAACG	1229 TGCTG       1232 CGCAG	1289 GTTTC      1292 ATTTC	1349 TCTGP   1352 CTTAG	1409 GGCAC 1412 AAACT	1469 GAGAG       1472 GAGAG	1529 GCTGC
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The invention relates to an isolated nucleic acid molecule encoding a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and capable of increasing salt tolerance in a cell. This sequence corresponds to the gene encoding a transporter from Arabidopsis thaliana. The Na/H transporter polypeptides provide a means of intracellular salt management, particularly in plants. The sequences are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sodium; proton; antiport; transporter; salt tolerance; salt management; transgenic plant; survival; soil; farming; accumulation; irrigation;
                                                                                                                                                                                                         1642 GCCATCCTGTC------ACCTCTGAGCCTTCATCACCAAAGTCCCTGCATTC 1687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1801
1592 TGTATTCGGGTTGATGACGAAGCCTCTGATAAACCTTCTGCTACCCCGCCACAAGCAGAT 1651
                                                                                                                                                                                                                                                                             1652 GCCAAGCGGTCATTCGTCAATGACAACATCCGAACCCAGTAGTCCGAAGCACTTCACGGT 1711
                                                                                                                                                                                                                                                                                                                                                                                                                  1712 GCCACTCCTGGACAACCAACCTGACTCAAAAGCGATATGATAACCGGACCTGAGGTTGC 1771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1742 GAGGCCTTCCAGCCTCCGGATGCTCCTCACCAAGCCGACCCACACTGTCCACTACTACTG
                                                                                                                                                                                                                                                                                                                                                     --ACATIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1589 GGTATTTGGGATGATGACAAAGCCATTGATCAGGCTGCTGCTACCGGC--
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                                                                                                                                                                                                                                                                                                                                                 1688 TCCTCTCCTGACAAGCATGCAAGGTTCTGACCTCGAGAGTACAACCA--
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(APSE/) APSE M.
(SNED/) SNEDDEN W.
(AHAR/) AHARON G.
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producing transgenic plants that are capable of surviving in soil with high salt levels that would normally inhibit growth of the crop species. This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and poor irrigation, e.g. in India, Australia, and prairies in USA or Canada. Commercial crops, such as potatoes, tomatoes, brassica, cotton, sunflower, strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley, atriplex, sorghum, alfalfa, salicornia and others would benefit from increased salt tolerance.
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                                                                                                                                                                                                                                                 Query Match 32.1%; Score 746.8; DB 20; Length 2284; Best Local Similarity 68.5%; Pred. No. 7.8e-196; Matches 1077; Conservative 0; Mismatches 487; Indels 8;
                                                                                                                                                                                                             Sequence 2284 BP; 589 A; 444 C; 485 G; 766 T; 0 other;
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The present sequence is a gene, which encodes a protein with vacuolar pH regulatory activities. The gene enables flower colour to be controlled via regulation of the vacuolar pH, colours can range from blue to red in colour spectrum. The gene is useful in controlling flower colour to give the breeds of colourful plants for cut flowers, particularly applicable
                                                                                                                                           Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable in
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2361 BP; 614 A; 468 C; 516 G; 763 T; 0 other;
                                                                                                                                                                                                                                       Example 7; Page 53-57; 68pp; Japanese.
                                                     Tanaka S, Inagaki Y;
                   SUNTORY LTD
                                                                                      WPI; 2001-191648/19
P-PSDB; AAB73254.
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GACCTCCGACTACGCGTCGTGCTCCATCAACCTGTTCGTCGCGCTGCTCTCGCGCCTG 400 Gaps 30.5%; Score 711.8; DB 22; Length 2361; 66.5%; Pred. No. 3.9e-186; ive 0; Mismatches 507; Indels 39; Best Local Similarity 66.5 Matches 1085, Conservative Query Match 341 ò

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GAGCTCTGGTCACGGTTCAGTGGTCGCTATAACCTTATTTGTCACTCTTCTCTGCACATG 508 CATCGTCCTCGGCCACCTCCTCGAGGAGAATCGCTGGGTCAATGAGTCCATCACCGCGCT 460 568 520 rererregieratica de accinitar de la contra dela contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra dela contra de la contra del la 509 TATAGIGATIGGICALCITCIGGAGGAAACCGITGGATGAATGAATCTATCATIGCCCT CATCATCGGGCTCTGCACCGGCGTGGTGATCTTGCTGATGACCAAAGGGAAGAGCTCGCA CATAATIGGTTTAGCCACGGGAGTTATAATCCTGTTAATAAGTGGTGGAAAAAGCTCCCA 449 629 401 569 521 191

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AAZ22592 standard; cDNA; 1788 BP AAZ22592 RESULT AXB

AAZ22592;

AGATTTTCTTG

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The invention relates to an isolated nucleic acid molecule encoding a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and capable of increasing salt tolerance in a cell. This sequence corresponds to the gene encoding the AtNHX2 transporter from Arabidopsis thaliana. The Na/H transporter polypeptides provide a means of intracellular salt management, particularly in plants. The sequences are useful for producing transgenic plants that are capable of surviving in soil with high salt levels that would normally inhibit growth of the crop species. This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and poor irrigation, e.g. in India, Australia, and prairies in USA or Canada. Commercial crops, such as potatoes, tomatoes, brassica, cotton, sunflower, atriplex, sorghum, alfalfa, salicornia and others would benefit from increased salt tolerance.
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                                                                                    Sodium; proton; antiport; transporter; salt tolerance; salt management; transgenic plant; survival; soil; farming; accumulation; irrigation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecules encoding sodium/proton transport polypeptides, useful in genetic engineering salt tolerance in crop plants
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                                                  Arabidopsis thaliana Na/H transporter gene AtNHX2
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                                                                                                                                                                  Arabidopsis thaliana.
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ABK12638 standard; cDNA; 1674 BP.
   ABK12638;
RESULT 10
ABK12638
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18-JUN-2002 (first entry)

DNA

encoding Physcomitrella patens Na+/H+ antiporter PpNHX1.

plant protectant, cytostatic, stress tolerance; plant defence activity, canker, gall, tumour; appressonium; pathogenic stress; herbicide; insecticide, acid rain; drought tolerance; plant hormone synthesis; ultraviolet tolerance; flower development; terpene synthesis; Plant; Na+/H+ antiporter; PpNHX1; expressed sequence tag; EST; gene plant organoleptic; ss.

Physcomitrella patens.

WO200216423-A2.

28-FEB-2002

24-AUG-2001; 2001WO-US26550

25-AUG-2000; 2000US-227974P.

(BADI ) BASF PLANT SCI GMBH.

Ishitani M; Da Costa Silva EO,

WPI; 2002-292058/33.

New Na+/H+ antiporter nucleic acids and proteins, useful e.g. for modulating stress tolerance in plants, or for detecting, preventing, conferring resistance to or treating hyperproliferative diseases, e.g. cankers, galls or tumours

Claim 1; Fig 2; 204pp; English.

process to the treatminteation and isotrated to that the polymuclectides or polypetides are further used to detect, prevent, confer resistance to and/or treat hyperproliferative diseases such as cankers, galls, tumours, and appressorium, increase of diseases such as cankers, galls, tumours, and appressorium, increase plant defence mechanisms against environmental or pathogenic stresses of e.g. viral, fungal, mycoplasma, bacterial, nematode, herbicidal, insecticidal, acid rain, drought, or chemical), and hormone synthesis. The Na+H+ antiporter coding nucleic acids can be used in creating transgenic plants with desirable traits, including enhanced plant certains including enhanced plant certains including enhanced plant companied to recombinant proteins to raise antibodies against polypeptides, as markers for tissues in which the corresponding protein is expressed, as chromosome markers or tags for chromosome mapping, and for genetic fingerprinting. The polypeptides are useful in the identification, prevention, and/or conferment of resistance to plant diseases, corresponding protein stress corresponding environmental stress responses, such as drought, freezing and salt tolerance. The polypeptides of particularly those associated with modulating environmental stress of environmental in madularing and for plant diseases. The invention relates to novel isolated Na+/H+ antiporter coding nucleic acid (I) and polypeptides (II). (I) and (II) are useful in modulating the stress toolerance in a plant, preferably modulating a plant's toolerance to limited or inadequate water availability, excess salt or osmotic conditions, excess temperature conditions, excess metal concentration in soil or water, chemical stress and oxidative stress. These may also be used as carbon, nitrogen or carbohydrate source, in modulating plant defence activity, signal transduction, or metabolite transport; or as probes for the identification and isolation of full length cDAAs or are further useful in modulating plant yield, development, differentiation, root growth, root morphology, plant colour, plant aroma, plant flavour, palatability of plant tissue, plant organoleptic properties, ability to serve as plant nutraceutical, pharmaceutical or phytoceutical, ability to produce nutraceutical, pharmaceuticals or phytoceuticals of either endogenous or exogenous origin. Antibodies may be used in diagnostic assays to detect the presence or quantity of the

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polypeptides, in affinity purification of the polypeptides from recombinant cell culture or natural sources, and for inhibiting allergic reactions in animals. The present sequence encodes Physcomitrella patens
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                                                                                                                                                                                                              11;
                                                                                                                                                                   Length 1674;
                                                                                                                                                                                      Pred. No. 7.8e-123;
0; Mismatches 462; Indels
                                                                                                                   Sequence 1674 BP; 426 A; 350 C; 361 G; 537 T; 0 other;
                                                                                                                                                              DB 24;
                                                                                                                                                                 20.7%; Score 482.8;
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                                                                        Na+/H+ antiporter PpNHX1.
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us-09-888-035a-1.rng

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Sodium, proton; antiport; transporter; salt tolerance, salt management; transgenic plant; survival; soil; farming; accumulation; irrigation;
                              1320 GGGATAAGCTCAATTTTGCTAGGATTGGTTCTGATTGGAAGAGCTGCTTTTGTATTCCCG 1379
                                                                                            1440 CAAGTTGTAATATGGTGGGCTGGGCTGATGAGAGGAGCTGTGTGGATTGCTCTTGCTTAC 1499
                                                                                                                                                                                           1217
                                                                                                                                                                                                                                                                                         1560 ACCATCACTGTCGTTCTTTTAGCACTATGGTATTTGGGATGATGACAAAGCCATTGATC 1619
979 ATGGATGCTCTGGATTTCGAAAAATGGAAGATGATGCAATCCAG-TTTCACGGAATCTGC 1037
                                                            CTCTCTGCTTTGTCCAACTACAGGACAAGTCTCCAGACGCGAAGATTAATTTACGCCAA 1157
                                                                                                                                                                                                                         1500 AATAAGTTTACAAGATCTGGCCATACTCAGCTGCACGGCAATGCAATAATGATCACCAGC 1559
                                                                                                                                                                                                                                                         1218 AACCAG-----GGTGGTGATGCAAAGGCTCAAACCAA-GCCACGCTAATGGTCATT 1267
                                                                                                                                                                                                                                                                                                          1268 ACTATCATCATTGTCCTCTTCAGCACTATTGTGTTTCGGCACTGCAACCAAGCCTCTTATT 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid molecules encoding sodium/proton transport polypeptides, useful in genetic engineering salt tolerance in crop plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid molecule encoding a plant NaTH antiport (PNHX) transporter polypeptide, or a fragment and capable of increasing salt tolerance in a cell. This sequence corresponds to an Na/H antiport transporter gene fragment from the rice expressed sequence tag (EST) library clone AAO91812. The Na/H management, particularly in plants. The sequences are useful for
                                                                                                                                                                                         1158 ATGGTTATTATCTGGTGGGCTGGACTAATGCGAGGTGCTGTCTCAATAGCACTGGCGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice Na/H antiport transporter gene from EST clone C91832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aharon G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 8C; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Snedden W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ22606 standard; DNA; 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-CA00219.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0116111
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                                                                                                                                                                                                                                                                                                                                                         1620 AGGCTGCTGCTACC 1633
                                                                                                                                                                                                                                                                                                                                                                                         1328 AGCTGGCTACTTCC 1341
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SNEDDEN W.
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producing transgenic plants that are capable of surviving in soil with high salt levels that would normally inhibit growth of the crop species. This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and poor irrigation, e.g. in India, Australia, and prairies in USA or Canada. Commercial crops, such as potatoes, tomatoes, brassica, cotton, sunflower, strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley, atriplex, sorghum, alfalfa, salicornia and others would benefit from increased salt tolerance.
                                                                                                                                                                                                                                                                 1013 CAAGAAGCTATACATTGGAAGGCATTCTACTGACCGTGAGGTTGCCCTTATGATGCTCAT 1072
                                                                                                                                                                                                                                                                                                                                  1073 GCCTTACCTTTCATATATGCTGGCTGAGTTGCTAGATTTGAGCGGCATTCTCACCGTATT 1132
                                                                                                                                                                                                                                                                                                                                                                                                  CTTCTGTGTGTATTGTAATGTCACATTACACTTGGCATAACGTCACAGAGAGTTCAAGAGT 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACAACAAAGCACGCATTTGCAACTCTGTCCTTCATTGCTGAGACTTTTCTTCTTCCTGTA 1252
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                                                                                                                                                                                                                                                                                                                                                                                                                     ATCCATTGGGATAAGCTCAATTTTGCTAGG--ATTGGTTCTGATTGGAAGAGCTGCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis Na/H antiport transporter gene from EST clone T75860
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                                                                                                                                                                                                 14.6%; Score 340.4; DB 20; Length 378; 95.0%; Pred. No. 8.7e-84;
                                                                                                                                                                                                                                   17; Indels
                                                                                                                                                                    Seguence 378 BP; 88 A; 74 C; 89 G; 121 T; 6 other;
                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ22611 standard; DNA; 330 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTATTCCCGCTGTCGTTC 1388
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99US-0116111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                    Matches 359; Conservative
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SNEDDEN W.
                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                    Query Match
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The invention relates to an isolated mucleic acid molecule encoding a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and capable of increasing salt tolerance in a cell. This sequence corresponds to an Na/H antiport transporter gene fragment from the Arabipdosis expressed sequence tag (EST) library clone AAT75860. The Analpdosis expressed sequence tag (EST) library clone AAT75860. The Na/H transporter polypeptides provide a means of intracellular salt management, particularly in plants. The sequences are useful for producing transgenic plants that are capable of surviving in soil with high salt levels that would normally inhibit growth of the crop species. This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and poor irrigation, e.g. in India, Australia, and prairies in USA or Canada. Commercial crops, such as potatoes, tomatoes, brassica, cotton, commercial crops, such as potatoes, tomatoes, brassica, cotton, rye, barley, atriplex, sorghum, alfalfa, salicornia and others would benefit from increased salt tolerance.
                                                                                                                                                 Nucleic acid molecules encoding sodium/proton transport polypeptides, useful in genetic engineering salt tolerance in crop plants
                                                      Aharon G;
                                                                                                                                                                                                                          Disclosure; Fig 8H; 93pp; English.
                                                 Snedden W,
                                                    Apse M,
                                                                                                  WPI; 1999-571840/48.
(AHAR/) AHARON G.
                                                    Blumwald E,
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o; Gaps . 0 6.0%; Score 139.2; DB 20; Length 330; 65.9%; Pred. No. 4e-28; Artive 0; Mismatches 101; Indels 0; Sequence 330 BP; 92 A; 68 C; 66 G; 91 T; 13 other; Matches 195; Conservative Local Similarity Query Match

1434 AGACAGCAAGTTGTAATATGGTGGGCTGGGCTGATGAGAGAGCTGTGTCGATTGCTCTT 1493 GCTTACAATAAGTTTACAAGATCTGGCCATACTCAGCTGCACGGCAATGCAATAATGATC 1553 AACATGCAGGTTGTGATTTGGTGGTCTCTCTCATGAGGTGCTGTATCTATGGCTCTTT 120 121 GCATACAACAAGTITACAAGGGCCGGGCACACAGATGTACGNGGGAATGCAATCATGATC 180 1 TTTCCGTTATCGTTTCTATCTAACTTAGCCAAGAAGAATCAAAGCGAGAAAATCAACTTT 60 61 1494 임 ò 셤 8

181 ACGNGTACGNTAACTGTCTGTNTTTTTAGCACAGTGGTGTTTGGTATGCTGACCAAACCA 240 TIGATCAGGCTGCTACCGGCCTCAGGCCATCCTGTCACCTCTGAGCCTTCATC 1669 241 NTCATAAGCTACCTATTTACCGNACCANGAACCGTCATCAACGNGGCATGTTTATC 296 1614 g ð 셤

ACCAGCACCATCACTGTCGTTCTTTTAGCACTATGGTATTTGGGATGATGACAAAGCCA 1613

1554

임 ò .. N

ABL73323 standard; cDNA; 281 BP.

ABL73323;

14-MAY-2002 (first entry)

Corn tassel-derived polynucleotide (cdps) SEQ ID NO:2697.

Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs; inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.

237 T--GGACATGAGAAGTGGAAATTAGCTAGTAGCAGTCCTAAGAAACC 281

AAC95372 standard; cDNA; 1824 BP

RESULT 14 AAC95372 ID AAC9

Zea mays

US2001051335-A1 

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The present sequence describes a purified corn tassel-derived
polynucleotide sequence (cdps) comprising a nucleic acid sequence
selected from those given in ABL70627 to ABL76833. The cdps sequences
cencede corn tassel-derived polypeptides (CDPs). The cdps sequences
can be used for determining altered gene expression, to recover
can be used for determining altered gene expression, to recover
central control of collow inheritance of desirable
characteristics through hybrid breeding programs. (I) are also useful
in the evaluation, and alteration of desired characteristics associated
with growth and development, disease resistance, environmental
adaptability, quality and yield, and as molecular markers for studying
contransoribity, quality and yield, and as molecular markers for studying
contransoribit image, to clone regulatory elements for use in transformation
centrol or express a polypeptide, to identify, isolate or extend
centrol or related corn tassel nucleic acid sequences from DNA
control or related corn tassel nucleic acid sequences from DNA
control or use in Southern or Northern hybridisation, and to identify the
corn use in Southern or Northern hybridisation, and to identify the
corn more) nucleic acid sequences.

Corn more) nucleic acid sequences.
                                                                                                                                                                                                                                                                                                                                               determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1029 GGAAGGCATTCTACTGACCGTGAGGTTGCCCTTATGATGCTCATGGCTTACCTTTCATAT 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1089 ATGCTGGCTGAGTTGCTAGATTTTGAGCGGCATTCTCACCGTATTCTTCTGTGGTATTGTA 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1149 ATGTCACATTACACTTGGCATAACGTCACAGAGGTTCAAGAGTTACAACAAAGCACGCA 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ATGATATCAATGCTGTTGGACCTGAGTGGAATTCTTACTGTCTTCTTCTGTGGAATAGTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 24; Length 281;
                                                                                                                                                                                                                                                                                                                        purified corn tassel-derived polynucleotide useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 138.8; DB 24; Lens.
Pred. No. 4.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1269 TTGGATATTGAAAATGGGAGTTTGCCAGTGACAGACCTGGCAAATC 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 281 BP; 83 A; 54 C; 56 G; 87 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 2697; 201pp; English.
                                                                                                                                                                                                                                         Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%;
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                                                             99US-0294093
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                                                                                                                                                (LALG/) LALGUDI R V.
                                                                                                                                                                         (ITOL/) ITO L Y.
(SHER/) SHERMAN B K.
                                                                                                                                                                                                                                                                               WPI; 2002-163647/21.
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                                                                                                                                                                                                                                                                                                                                                                                            breeding programs
                                                             16-APR-1999;
                                                                                                        21-APR-1998;
                    13-DEC-2001.
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Wed Apr

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AAC95372;
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Cat flea HMT Na/H transporter cDNA ORF, SEQ ID NO:1870.

(first entry)

19-FEB-2001

Cat flea; hindgut and Malpighian tubule nucleic acid; HMT; flea infestation; vaccine; antiparasitic; therapeutic target; diagnosis; detection; ss.

Ctenocephalides felis.

WO200061621-A2

19-OCT-2000

07-APR-2000; 2000WO-US09437.

99US-0128704 19-APR-1999;

(HESK-) HESKA CORP

Stinchcomb DT, Wisnewski N; Brandt KS, Gaines PJ,

WPI; 2000-656323/63. P-PSDB; AAB29621.

Flea Malpighian tubule and head and nerve cord tissue derived nucleic acids useful for the prevention, diagnosis and treatment of flea

Claim 1; Page 894-895; 964pp; English.

infestations

The invention relates to novel cat flea (Ctenocephalides felis) nucleic acids which are expressed in hindgut and Malpighian tubule (HMT) tissue or head and nerve cord (HMC) tissue. The invention also relates to the encoded proteins. The invention additionally encompasses expression constructs, recombinant viruses and recombinant cells comprising the nucleic acids of the invention, recombinant production of the proteins, and compositions comprising the inhibitors of the proteins, and compositions comprising the inhibitors of administration to an animal. The nucleic acids, and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with flea infestations. For example, the nucleic acids may associated with flea infestations. For example, the nucleic acids may used to produce an HMT or HMC protein according to standard recombinant culturing the cell to express the protein. The HMT and HMC nucleic acids may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect and quantitate the presence of cat files or other homologus nucleic acid and quantitate the presence of cat files or other homologus nucleic acid function of the proteins and their role in metabolism. The HMT and HNC protein may be used as antigens in the production of specific and and in a samples. used as diagnostic agents for detecting the presence of flea polypeptides in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The present sequence represents a cat flea HMT cDNA of the invention. antibodies, and in assays to identify modulators (agonists and antagonists) of HMT and/or HNC protein expression and activity. The anti-HMT/HNC protein antibodies and antagonists may also be used to downregulate protein expression and activity. The antibodies may also be

Sequence 1824 BP; 529 A; 330 C; 355 G; 610 T; 0 other;

ij 4.7%; Score 109.4; DB 21; Length 1824; 47.8%; Pred. No. 1.9e-19; 3; 0; Mismatches 381; Indels Matches 351; Conservative Local Similarity Query Match

TICTICATCTACCTCCTCCCATCATCTTCAATGCAGGTTTTCAGGTAAAAAAA 605 445 Trrircriagrecfrcraccecrataararraaarcceegraraarrigcaraaaggr 504 546 g ઠે

606 CAATTCTTCCGGAATTTCATGACGATCACATTATTTGGAGCCGTCGGGACAATGATATCC 665 ò

1023 TACATTGGAAGGCATTCTACTGACGTGAGGTTGCCCTTATGATGCTCATGGCTTACCTT 1082 1143 ATTGTAATGTCACATTACACTTGGCATAACGTCACAGAGGTTCAAGAGTTACAAAAG 1202 1045 ATTGTGATGTCCCATTACACACTTTCAATTATCAACGGTTACACAAATAACTATGCAG 1104 CACGCATTIGCAACTCTGTCTTCATTGCTGAGACTTTTCTCTTCTGTATGTTGGGATG 1262 1105 cagacgargagaacrrrrggcrrrrarrgcagaaacrrgrgrgrrrgcrrarraggaarg 1164 985 ccriarcitiridecadaagaarircaititarcaderaraargecgararriticididec 1044 842 902 962 805 CCTTTAATGACGACTGCTGAAGCTGTAGTCTCCGGTTTTAAATAGGTTTTAATGTTTAATGTTC 864 865 TTTGCTTCGGCTGGTATCGGTGTAGTCTTTTGCCTTAATTAGTGCTCTTTTGTTGAAACAT 924 925 GTTGATCTTAGAAAGTATCCGTCCTTAGAGTTAGGTATGATGTTGGTGTTTACTTATGCA 984 666 TITITCACAATATCTATTGCTGCCATTGCAATATTCAGCAGAATGAACATTGGAACGCTG 725 625 AGCTTTGTTGAATCCTTTGCTTTCGGTTCATTAATTTCTGCAGTAGACCCTGTAGCTACC 684 685 GIAGCIAITIICCAIGCIIIAGACGIGGACCCAGIIIIIAAACAIGIIGGIGIIICGGAGAA 744 745 AGTATTTTAAATGATGCTATTTCAATTGTTTTAACAACTGCAGTTTTGGAATCCAACAAT 804 505 AATTITITICAAAATATIGGITCCATCCTGGIGITIGCTATATITIGGAACAGCCATAICA 564 565 GCCTTTGTTGTTGTGTGCTGGTGTGTATTTACTAGGAATGGCAGATGTTGCTTATAACTTA 786 TTGCAGGTCCTCAA---TCAGGATGAGACACCCTTTTTGTACAGTCTGGTATTCGGTGAA 1083 TCATATATGCTGGCTGAGTTGCTAGATTTGAGCGGCATTCTCACCGTATTCTTCTGTGGT 843 GGTGTTGTGAACGATGCTACATCAATTGTGCTTTTCAACGCACTACAGAACTTTGATCTT 903 GICCACATAGAIGCGGCIGICGTICIGAAAIICITGGGGGAACTICITITAIITATITITG 1263 GATGCATTGGATATT 1277 1165 GCTATATTTAGTTTT 1179 963 1203 8 g q ò g ò q ò 셤 ò П ò g ò ð g ò g ò ð

RESULT 15 AAC95373,

AAC95373 standard; cDNA; 1824 BP.

AAC95373; 

(first entry) 19-FEB-2001 Cat flea HMT Na/H transporter cDNA ORF complement, SEQ ID NO:1871.

Cat flea; hindgut and Malpighian tubule nucleic acid; HWT; flea infestation; vaccine; antiparasitic; therapeutic target; diagnosis; detection; ss.

Ctenocephalides felis

WO200061621-A2

19-OCT-2000

07-APR-2000; 2000WO-US09437.

99US-0128704 09-APR-1999;

(HESK-) HESKA CORP.

Stinchcomb DT, Wisnewski N; Gaines PJ, Brandt KS,

WPI; 2000-656323/63.

P-PSDB; AAB29621

Flea Malpighian tubule and head and nerve cord tissue derived nucleic acids useful for the prevention, diagnosis and treatment of flea infestations -

Claim 1; Page 895-896; 964pp; English.

The invention trainers to novel cat thes (Cenocophaliose Felis) nucleic acids which are expressed in hindgut and Malpighian tubule (HMT) tissue or head and nerve cord (HMC) tissue. The invention also relates to the encoded proteins. The invention additionally encompasses expression constructs, recombinant viruses and recombinant cells comprising the nucleic acids of the invention, recombinant production of the proteins, and the proteins, and compositions comprising the inhibitors of the proteins, and compositions comprising the inhibitors of administration to an animal. The nucleic acids, and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with flea infestations. For example, the nucleic acids may be used to produce an HMT or HMC protein according to standard recombinant DNA methodology by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The HMT and HMC nucleic acids and quantitate the presence of cat flea or other homologous nucleic acid sequences in samples. They may also be used to study the expression and tunction of the proteins and their role in metabolism. The HMT and HMC proteins and their role in metabolism. The HMT and HMC proteins may be used as antigens in the production of specific acids antigonists and ain assays to identify modulators (agonists and antigonists) of HMT and/or HMT protein expression and activity. The antigonists of the protein expression and activity. anti-HMT/HNC protein antibodies and antagonists may also be used to downregulate protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of flea polypeptides in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The present sequence represents a cat flea HMT cDNA of the invention. invention relates to novel cat flea (Ctenocephalides felis) nucleic

Sequence 1824 BP; 610 A; 355 C; 330 G; 529 T; 0 other;

1380 TITITCTTAGTGCTTCTACCGCCTATAATATTTGAATCCGGGTATAATTTGCATAAAGGT 1321 1320 AATTTTTTTTCAAATATTGGTTCCATCCTGGTGTTTGCTATTTTGGAACAGCCATATCA 1261 1200 AGCTÍTGTTGAAÍCCTÍTGCTTÍCGGTTCATÍAAÍTÍTCTGCAGTÁGACCCTGTAGCTÁCC 1141 1080 AGTATTTTAAATGATGCTATTTCAATTGTTTTAACAACTGCAGTTTTGGAATCCAACAAT 1021 1260 GCCTTTGTTGTGGGGGGGGGGGGTTTTACTAGGAATGGCAGATGTTGCTTATAACTTA 1201 1140 GTAGCTATTTTCCATGCTTTAGACGTGGACCCCAGTTTTAAACATGTTGGTGTTCGGAGAA 1081 546 TICTICALCIACCICCICCCICCGALCATCITCAAIGCAGGITITICAGGIAAAAAG 605 606 CAATTCTTCCGGAATTTCATGACGATCACATTATTTGGAGCCGTCGGGACAATGATATCC 665 666 TITITCACAATAICTATIGCTGCCATIGCAATATTCAGCAGAATGAACATIGGAACGCTG 725 786 TTGCAGGTCCTCAA---TCAGGATGAGACACCCTTTTTGTACAGTCTGGTATTCGGTGAA 842 1020 CCTTTAATGACGACTGCTGAAGCTGTAGTCTCCGGTTTAAATAGGTTTTAATGTTC 961 3; Gaps 843 GGTGTTGTGAACGATGCTACATCAATTGTGCTTTTCAACGCACTACAGAACTTTGATCTT 4.7%; Score 109.4; DB 21; Length 1824; 47.8%; Pred. No. 1.9e-19; ative 0; Mismatches 381; Indels 3; Best Local Similary, Matches 351; Conservative Similarity Query Match g g à ò ઠે g δ 8 셤 ò ð

QQ	096	TTTGCTTCGGCTGGTATCGGTGTAGTCTTTGCCTTAATTAGTGCTCTTTTGTTGAAACAT 901
δλ	1023	TACATTGGAAGGCATTCTACTGACCGTGAGGTTGCCCTTATGATGCTCATGGCTTACCTT 1082
qq	900	GTTGATCTTAGAAAGTATCCGTCCTTAGAGTTAGGTATGATGTTGGTGTTTACTTATGCA 841
Ολ	1083	TCATATATGCTGGCTGAGTTGCTAGATTTGAGCGGCATTCTCCACGTATTCTTCTGTGGT 1142
qq	840	CTIATGTTTTGGCAGAAGGAATTCATTTATCAGGTATAATGGCGATATTATTGTTGTGGC 781
δλ	1143	ATTGTAATGTCACATTACACTTGGCATAACGTCACAGAGAGTTCAAGAGTTACAACAACAAG 1202
qq	780	ATTGTGATGTCCCATTACACATTTCAATTTATCAACGGTTACAAAAAAATAACTATGCAG 721
δy	1203	CACGCATITGCAACTCTGTCCTTCATTGCTGAGACTTTTCTCTCTTCTGTATGTTGGGATG 1262
QQ	720	CAGACGAIGAGAACTITGGCITITATIGCAGAAACTIGIGIGITIGCTIAITIAGGAAIG 661
δλ	1263	GATGCATTGGATATT 1277
qq	099	GCTATATTTAGTTTT 646
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on:

April 5, 2003, 12:44:33 ; Search time 92 Seconds (without alignments) 7766.922 Million cell updates/sec

Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

441362 segs, 153338381 residues Searched: Total number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued\_Patents NA:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			d				
Result	ılt		Query				
Z	No.	Score	Match	Length	BB	di	Description
	٦	62.6	2.7	2574	5	US-08-677-734A-8	Sequence 8, Appli
	7	62.6	2.7	2574	4	US-09-097-053-8	8
υ	m	44.6	1.9	3489	~	US-08-728-323A-1	H
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	13	39.6	1.7	7218	7	US-08-232-463-14	14
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	22	38.8	1.7	1833	7	US-08-403-852D-6	Sequence 6, Appli
	23	38.8	1.7	1833	m	US-08-510-646B-6	9
	24	38.8	1.7	1833	4	US-09-231-818-6	Sequence 6, Appli
υ	25	38.6	1.7	795	~	US-08-997-080-46	46,
υ	56	38.6	1.7	795	7	US-08-997-362-46	46,
υ	27	38.6	1.7	795	c	US-08-873-970-46	46,

Sequence 46, Appl Sequence 46, Appl Sequence 46, Appl Sequence 46, Appl Sequence 11, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli
US-09-095-855-46 US-09-324-542-46 US-09-324-542-46 US-09-200-643-46 US-09-200-643-46 US-08-604-789B-1 US-08-604-789B-1 US-08-112-721A-1 US-09-312-721A-1 US-09-312-721A-1 US-08-7-852-132A-12 PCT-1051-01327-12 PCT-1051-01327-12 US-08-005-005-3 US-08-005-005-3 US-08-005-005-3 US-08-005-005-3 US-08-005-005-3 US-08-166-738-2 US-08-789-915A-3 US-08-166-738-2 US-08-76-738-2
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## ALIGNMENTS

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JEACH NO. CHIS C.H.

APPLICANT: BEACK, MARK

APPLICANT: TUN, Chris C.H.

APPLICANT: Coning-Ming

JITLE OF INVENTION: Cloning, Tissue Distribution, and

JITLE OF INVENTION: Cloning, Tissue Distribution, and

JITLE OF INVENTION: Chris C.H.

ADDESSES: Pinnegan, Henderson, Farabow, Garrett &

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CLASSIFICATION NUMBER: US/08/677,734A

APPLICATION NUMBER: US/08/677,734A

APPLICATION NUMBER: US/08/677,734A

APPLICATION NUMBER: US/08/677,734A

ARTOREY/AGENT INFORMATION:

MANG: FORCET NUMBER: US/08/6400

TELECOMMUNICATION INFORMATION:

NAME: FORCET SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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EDNESS: single
US-08-677-734A-8
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Gaps

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TOPOLOGY:
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Patent No. 6392025
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: From Chris C.H.
APPLICANT: From Chris C.H.
APPLICANT: OF INVENTION:
TITLE OF INVENTION: Cloning, Tissue Distribution, and
TITLE OF INVENTION: Punctional Analysis of The Human Na+/H+ Exchanger Isoform,
TITLE OF INVENTION: NHE3.
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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44.8%; Pred. No. 9e-08;
Live 0; Mismatches 399; Indels 9
                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,053 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05387.0043-00000
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/677,734
FILING DATE: 10-UUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: FOCTIS, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387
TELECOMMUNICATION INPORMATION:
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: DNA (genomic) US-09-097-053-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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1135 TCTGTGGTATTGTAATGTCACATTACACTTGGCATAACGTCACAGAGAGTTCAAGAGTTA 1194
                                          941 TCTGTGGCATCTGCTGTCAGAAGTATGTGAAGGCCAACATCTCGGAGCAGTCGGCCACCA 1000
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Patent No. 5948676

GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Brocding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.9%; Score 44.6; DB 2; Length 3489; 50.7%; Pred. No. 0.017; tive 0; Mismatches 104; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                 1255 TTGGGATGGATGCATTGGA 1273
                                                                                                                                                                                                                            1061 TGGGTATCTCGGCCGTGAA 1079
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SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 107; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 1...
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GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
CURRENT PILLING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
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                                                       1129 CATCCTCCTCGTCATCCTCCTCGTCATCCTCGTCATCCTCCTCGTCGTCATCCTCCTCGT 1070
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488 GATCTTGCTGATGACCAAAGGGAAGAGCTCGCACTTATTCGTCTTCAGTGAGGATCTCTT 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Kaposi's sarcoma-associated herpesvirus
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Fatent No. 5849564
GENERAL INFORMATION
APPLICANT: Chang, Yuan
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Roore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAI, TITLE OF INVENTION: HERPESVIRUS, DNA ENCY; TITLE OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1069 carcercercarcarcercercarcarcic 1039
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Patent No. 6322792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                    RESULT 4
US-09-298-568-1/c
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US-08-770-379-20
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APPLICATION NUMBER: US/08/757,669A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.9%; Score 44.6; DB 2; Length 32207; Best Local Similarity 50.7%; Pred. No. 0.065; Matches 107; Conservative 0; Mismatches 104; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Partick S.
APPLICANT: Moore, Partick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOST'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
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ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/08757669A; Patent No. 6183751; GENERAL INFORMATION: APPLICANT: Chang, Yuan
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION UNDRER: 28,678
REFERENCE/DOCKET UNDRER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                   32207 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: double
                                                                                                                                                                                                             CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                    FILING DATE:
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US-08-757-669A-20
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APPLICANT: Chang, Yuan
APPLICANT: Bohelzky, Roy A
APPLICANT: Bohelzky, Roy A
APPLICANT: But Belling, Isidore S
APPLICANT: Belling, Isidore S
APPLICANT: Moore, Patrick S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THEREOF
FILE REFERRENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR PILING DATE: 1999-11-17
PRIOR PLING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-F
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-09-230-371A-20
; Sequence 20, Application US/09230371A
; Patent No. 6348586
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US-08-757-669A-20
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Best Local Similarity 50.7%
                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                      linear
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APPLICANT: Chang, 1
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SEQ ID NO 20
LENGTH: 32207
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                                                  20808 CCTCCTCCTCGTCCTCCTCGTCCTCCTCCTCGTCATCCTCCTCGTCATCCTCCTCGT 20867
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428 GAATCGCTGGGTCAATGAGTCCATCACCGCGCTCATCATCGGGCTCTGCACCGGCGTGGT 487
                                                                                                    488 GATCTTGCTGATGACCAAAGGGAAGAGCTCGCACTTATTCGTCTTCAGTGAGGATCTCTT 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 CTCCTCGAGGAGAATCGCTGGGTCAATGAGTCCATCACCGCGCTCATCATCGGGCTCTGC 476
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                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Rudolf Jung
APPLICANT: Rudolf Jung
APPLICANT: Prancois Barrieu
ITILE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR APPLICATION NUMBER: US 60/098,692
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
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Sequence 14, Application US/08232463

Sequence 11, Application US/08232463

GENERAL INFORMATION:
APPLICANT: BORNER, F.
APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.8%; Score 42.8; DE
Best Local Similarity 51.6%; Pred. No. 0.027
Matches 98; Conservative 0; Mismatches
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                                                                                                                                                                                                      CTTCATCTACCTCCTCCCTCCGATCATCTTC 578
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Patent No. 6313375
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; LOCATION: (94)...(835)
US-09-372-422A-47
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ORGANISM: Zea mays
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1881 GAGCAGAGCCATGGAGGAAGATGAACAGTGCAAAGAAATGAAATGGAATGCTTGATGAG 1940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.8%; Score 42.4; DB 1; Length 7218; Best Local Similarity 4.4%; Pred. No. 0.11; Matches 13; Conservative 165; Mismatches 116; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCORNATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
APPLICANT: Geselach, Joern
ITILE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30592A
                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PEDLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                              29,768
3R: 30472/114 IMMU
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                                                                                                                                                                                                                                                                                                                  EP 91 114 300.6
                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                               FILING DATE:
PILING DATE:
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/09335409
; Patent No. 6121029
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
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US-09-335-409-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                     371 CAACCTGTTCGTCGCGCTGCTCTGCGCCTGCATCGTCCTCGGCCACCTCGTCGAGGAGA 430
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APPLICANT: Schupp, Thomas
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Gerlach, Joern
TILE OF INVENTION: GERES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT FILING DATE: 2000-05-10
PRIOR PRILICATION NUMBER: 09/335,409
PRIOR PAPLICATION NUMBER: 09/335,409
PRIOR PLING DATE: 1999-06-17
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49.5%; Pred. No. 0.44;
tive 0; Mismatches 111; Indels 0;
                                                                                                                                                                                                                             Query Match 1.8%; Score 42.4; DB 3; Length 6
Best Local Similarity 49.5%; Pred. No. 0.44;
Matches 109; Conservative 0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4530 GCICCICTCCAACGÁGGCTTATACGATGTACGCCGTCGTC 4569
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Patent No. 6346404
CURRENT FILING DATE: 1999-06-17
UNDBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
                                                                                                                         TYPE: DNA ORGANISM: Sorangium cellulosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Sorangium cellulosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 49.5
Matches 109; Conservative
                                                                                                      LENGTH: 68750
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                                                                                                                                                                             US-09-335-409-1
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                                                                                             GENERAL NO. 0533340;
GENERAL NO. 0533340;
GENERAL SCHUPD, Thomas
FAPPLICANT: Schupp, Thomas
FAPPLICANT: Light, Ross
FAPPLICANT: Grann
FAPPLICANT: Grann
FAPPLICANT: Grann
FAPPLICANT: Grann
FAPPLICANT: Grann
FILE REFERENCE: 4.3062A
FURBENT APPLICANTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 2000-05-10
FRIOR PEPLICANTION NUMBER: US/09/567,969
CURRENT FILING DATE: 1999-06-17
FRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOSTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 42.4; DB 4; Length 68750; 49.5%; Pred. No. 0.44;
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APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,480
CURRENT FILING DATE: 2000-05-10
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PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
                                                    Sequence 1, Application US/09567969
Patent No. 6355457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09568480; Patent No. 6355458; GENERAL INFORMATION:
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; ORGANISM: Sorangium cellulosum
US-09-568-480-1
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Molnar, Istvan
Zirkle, Ross
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SEQ ID NO 1
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LENGTH: 68750
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RESULT 12
US-09-567-969-1
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APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
TITLE OF INVENTION: Goether, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT FILING DATE: 2000-05-10
PRIOR PRILING DATE: 2000-05-10
PRIOR PLLING DATE: 1999-06-17
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               DB 4; Length 68750;
          Query Match 1.8%; Score 42.4; DB 4; Length 6. Best Local Similarity 49.5%; Pred. No. 0.44; Matches 109; Conservative 0; Mismatches 111; Indels
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US-09-568-472-1
Sequence 1, Application US/09568472
; Patent No. 6358719
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Patent No. 6355459
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; ORGANISM: Sorangium cellulosum
US-09-568-486-1
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SEQ ID NO 1
LENGTH: 68750
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US-09-568-486-1
Query Match
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                                                                            APPLICANT: Cyr, Devon
APPLICANT: Gerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FITLE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,472
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
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49.5%; Pred. No. 0.44;
tive 0; Mismatches 111; Indels 0;
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Job time : 288 secs
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Matches 109; Conservative
                                          Molnar, Istvan
Zirkle, Ross
Schupp, Thomas
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                                                                  APPLICANT:
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April 5, 2003, 14:52:33 ; Search time 210 Seconds (without alignments) 9732.385 Million cell updates/sec

US-09-888-035A-1 2330 Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters:

593429 segs, 438583890 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA:\*

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10: /cgn2\_6/ptodata/2/pubpna/USO9\_NEW\_PUB.seq:\*
11: /cgn2\_6/ptodata/2/pubpna/USO9\_NEW\_PUB.seq:\*
11: /cgn2\_6/ptodata/2/pubpna/USO9\_NEW\_PUB.seq:\*
13: /cgn2\_6/ptodata/2/pubpna/USO9\_NEW\_PUB.seq:\*
14: /cgn2\_6/ptodata/2/pubpna/USO9\_NEW\_PUB.seq:\*
14: /cgn2\_6/ptodata/2/pubpna/USO0\_NEW\_PUB.seq:\*
14: /cgn2\_6/ptodata/2/pubpna/USO0\_NEW\_PUB.seq:\*
14: /cgn2\_6/ptodata/2/pubpna/USO0\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		dр				
Result	2000	Query	Query	ä	4	Description
		יומרכזו		3		Description.
1	1 768.8	33.0	1617	6	US-09-938-842A-1239	Seguence 1239, Ap
N	2 766.8	32.9	2136	σ	US-10-155-535-1	Sequence 1, Appli
m	3 711	30.5	2066	σ	US-10-155-535-3	Sequence 3, Appli
4	138.8	9.9	281	10	US-09-294-093B-2697	Sequence 2697, Ap
u1	5 77	3.3	1800	σ	US-10-155-535-5	Sequence 5, Appli
Ψ	9.99	2.9	1688	10	US-09-800-729-57	Sequence 57, Appl
•	7 65	2.8	1581	10	US-09-800-729-22	Sequence 22, Appl
υ	3 58.4	2.5	4598	٠.	US-09-822-846-118	Sequence 118, App
U1	52.4	2.5	1354	10	US-09-800-729-58	
10	51.4	2.2	1935	σ	US-10-217-096-3	Sequence 3, Appli
11	1 51.4	2.2	3537	σ	US-10-217-096-1	Sequence 1, Appli
12	2 44.4	1.9	1305	10	US-09-815-242-7730	Sequence 7730, Ap
13	3 43.4	1.9	1883	12	US-10-033-109-9	Sequence 9, Appli
14	4 43	1.8	069	10	US-09-887-576-816	Sequence 816, App
15	5 42.6	1.8	325	0	US-10-040-739-929	Sequence 929, App
16	5 42.6	1.8	88421	σ	US-09-976-059-1	Sequence 1, Appli
17	7 42.4	1.8	68750	σ	US-10-014-717-1	Sequence 1, Appli
16	3 41.2	1.8	1827	10	US-09-887-576-817	Sequence 817, App
c 19	9 41	1.8	520	6	US-10-184-644-332	Sequence 332, App

8 8 4 11 E 6 6 8 9 6 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Sequence 3, Appli Sequence 46, Appli Sequence 46, Appl Sequence 1, Appli Sequence 12, Appli Sequence 12, Appli Sequence 949, Appli Sequence 949, Appli
US-09-815-242-7872 US-10-184-644-78 US-10-125-237-11 US-10-125-237-11 US-10-106-950-1 US-10-106-950-1 US-09-805-467A-1 US-09-805-467A-1 US-09-805-467A-1 US-09-805-467A-1 US-09-805-781 US-10-03-673-3 US-10-03-673-3 US-10-03-673-3 US-10-03-673-1 US-09-864-761-23962 US-09-864-761-23962 US-09-864-761-2825	US-09-927-091-3 US-09-927-091-7 US-09-800-505-46 US-09-733-300-1 US-09-733-300-12 US-09-733-300-12 US-09-834-975-949 US-09-834-975-949
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## ALIGNMENTS

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Sequence 1239, Application US/09938842A
Patent No. US20020160378A1
GENERAL INCOMMATION:
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Zhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFRENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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                                                                                                                                                                                                                                                                       PRIOR PLING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1239
LENGTH: 1617
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                                                             GATCATCTTCAATGCAGGTTTTCAGGTAAAGAAAAAGCAATTCTTCCGGAATTTCATGAC
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Sequence 1, Application US/10155535
Publication No. US20030046729A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blumwald, Eduardo
APPLICANT: Apse, Maris
TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
TITLE OF INVENTION: EXPRESSION OF VACUOLAR CATION-PROTON ANTIPORTERS
FILE REPERENCE: 529152000720
CURRENT FILING DATE: 2002-05-24
CURRENT TILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-01-15
SEQ ID NOS: 27
SEQ ID NO 1
GGTATTTGGGATGATGACAAAGCCATTGATCAGGCTGCTGCTACCGGCCTCAGGCCATCC 1648
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                                          1287 GGTGTTTGGTATGCTGACCAAACCACTCATAAGCTACCTATTACCGCACCAGAACGCCAC
                                                                                             1649 TGTCACC-----TCTGAGCCTTCATCACCAAAGTCCCTGCATTCTCCTCTCTGACAAG
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Best Local Simi
Matches 1088;
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Sequence 3, Application US/10155335

Publication No. US20030046729A1

GENERAL INFORMATION:
APPLICANT: Blumwald, Eduardo
APPLICANT: Blumwald, Eduardo
APPLICANT: Apse, Maris
ITILE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
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TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
TITLE OF INVENTION: INCREASING SALT TOLERANCE APPLICATION NUMBER: US/10/155,535
CURRENT FILING DATE: 1090-05-24
PRIOR PELING DATE: 1999-01-18
PRIOR PELING DATE: 1999-01-18
PRIOR PILING DATE: 1999-01-15
NUMBER: 60/116,111
PRIOR FILING DATE: 1999-01-15
NUMBER: FSELSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2066
-ACATTGTGAGGCCTTCCAGCC 1755
                                                                     1784 AACAGCTAGATTCATTTGAGTTACCTGGGAGCCACCAGGACGTGCCACGACCAAACAGCC 1843
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APPLICANT:

APPLICANT:

APPLICANT: Laura, Y.

APPLICANT: Sherman, Bradley, K.

ITLE OF INVENTION: POLYNCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL, FILE OF INVENTION: POLYNCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL, FILE OF INVENTION: POLYPEPTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL, FILE OF INVENTION: DATE: 1999-04-16

PRIOR REPLICATION NUMBER: 60/082,567

PRIOR FILING DATE: April 21, 1998

NUMBER OF SEQ ID NOS: 6207

SOFTWARE: PERL PROGRAM

SEQ ID NO 2697
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Sequence 5, Application US/1015535
PUBLICATION NO. US20030046729A1
GENERAL INFORMATION:
APPLICANT: Blumwald, Eduardo
APPLICANT: Apse, Maris
APPLICANT: NORMATION:
TITLE OF INVENTION: EXPRESSION OF VACUOLAR CATION-PROTON ANTIPORTERS;
TITLE OF INVENTION: EXPRESSION OF VACUOLAR CATION-PROTON ANTIPORTERS
                                                                        1834 TGTTTGGCGGGCGGGGTTCGTGCCCTTCTCCCCTGGATCACCAACCGAGCAAGAGCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700346512H1
NAME/KEY: unsure
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OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2697, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
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; Sequence 22, Application US/09800729
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                                                                                                                                                                                                                                                                                                                                              Score 77; DB 9; Length 180
Pred. No. 5.2e-13;
0; Mismatches 395; Indels
          CURRENT APPLICATION NUMBER: US/10/155,535
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 09/271,584
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1998-03-18
PRIOR PLILING DATE: 1998-03-18
PRIOR PLILING DATE: 1998-03-18
PRIOR PLILING DATE: 1998-01-15
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 5
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                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-155-535-5
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Best Local Similarity 45.9%;
FILE REFERENCE: 529152000720
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1085 ATATATGCTGGCTGAGTTGCTAGATTTGAGCGGCATTCTCACCGTATTCTTCTGTGGTAT 1144
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                                                Sequence 57, Application US/09800729
Patent No. US20020068319A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: PZ044P1
                                                                                                                                                                                          FILE REFERENCE: PZ044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR PILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PALENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (99)
; OTHER INFORMATION: n equals a,t,g, or
US-09-800-729-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or
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OTHER INFORMATION: n equals
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ORGANISM: Homo sapiens
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LENGTH: 1688
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RESULT 6
US-09-800-729-57
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Resnick, Richard J.
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Treacy, Maurice
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Fechtel, Kim
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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Pred. No. 2.7e-09;
6; Mismatches 367; Indels
                                                                                                                  32 Human secreted proteins
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted prote:
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT APPLICATION NUMBER: PCT/US00/26013
FRIOR APPLICATION NUMBER: PCT/US00/26013
FRIOR FILING DATE: 2000-09-22
FRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
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LOCATION: (112)
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LOCATION: (959)
OTHER INFORMATION: n equals a,t,g,
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Best Local Similarity 46.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: SITE
) LOCATION: (1565)
) OTHER INFORMATION:
US-09-800-729-22
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                                                                        1022 GAAGCCTGCGGATTTACAGGTGTTGTAGCTGTCCTTTTCTGTGGAATCACACAAGCTCAT 1081
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                                                                                                                                                1158 TACACTTGGCATAACGTCACAGAGAGTTCAAGAGTTACAACAAAGCACGCATTTGCAACT
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Steininger II, Robert J.
Bowman, Michael R.
Spaulding, Vikki
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PRIOR APPLICATION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 118
LENGTH: 4598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 118, Application US/09822846 Publication No. US20030027139A1
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Graham, James R.
Genetics Institute, Inc.
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LaVallie, Edward R.
Collins-Racie, Lisa A.
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3779 GCAACTGATCCAGTGACTGTTCTTGCTATATTCCACGAGCTTCAAGTTGATGTTGAACTC 3720
                                                                                        3719 TATGCACTTCTTTTTGGTGAAAGTGTCCTCAATGATGCTGTTGCCATAGTGCTGTCCTCC 3660
                                                                                                                                                                                                                                                                                                                               987 GCTGGATTGCTCAGTGCATACATAATCAAGAAGCTATACATTGGAAGGCATTCTACTGAC 1046
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Patent No. US20020068319A1
                                                                                                                                         882 GCACTACAGAACTTTGATCTTG----
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Matches 113; Conservative
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CORGANISM: Homo sapiens
US-09-800-729-58
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                                                                                                                                                                                                              APPLICAT: Curties, Rory A.J., Ferriera, Holly M.
TITLE OF INVENTION: 96895, A Human Sodium-Hydrogen Exchanger
TITLE OF INVENTION: Pamily Member and Uses Therefor
FILE REFERENCE: MP101-147PIRM
CURRENT APPLICATION NUMBER: US/10/217,096
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ 1D NOS: 7
SOFTWARE: FASTSEQ for Windows Version 4.0
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Best Local Similarity 46.2%; Pred. No. 5.9e-05;
Matches 350; Conservative 0; Mismatches 371; Indels
1230 GCTGAGACTTTTCTCTTCCTGTATGTTGGGATGG 1263
                                       198 GCAGAGACTTCATCTTCTCCTACATGGGCCTGG
                                                                                                                                                 Sequence 3, Application US/10217096 Publication No. US20030044933A1 GENERAL INFORMATION:
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US-10-217-096-3
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1107 GATTIGAGCGGCAITCICACCGTATTCTTCTGTGGTATTGTAATGTCACATTACACTTGG 1166
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Publication No. US20030044933A1
Publication No. US20030044933A1
Publication No. US20030044933A1
TERECONSTRUCTOR CURTIS, Rory A.J., Ferriera, Holly M.
TITLE OF INVENTION: 96895, A Human Sodium-Hydrogen Exchanger
TITLE OF INVENTION: Family Member and Uses Therefor
FILE REFERENCE: MPIOL-147P1RM
CURRENT APPLICATION NUMBER: US/10/217,096
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 9.2e-05;
0; Mismatches 371; Indels
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US-10-217-096-1
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Best Local 8
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987 GCTGGATTGCTCAGTGCATACATAATCAAGAAGCTATACATTGGAAGGCATTCTACTGAC 1046
                                                                                                                              GCGTATGCCATCATCACCAGCACTGTTGACCAAATTTACCAAGCTGTGTGAGTTCCCGATG 1011
                                                                                                                                                                                                                                                             GATTTGAGCGCCATTCTCACCGTATTCTTCTGTGGTATTGTAATGTCACATTACACTTGG 1166
                                                                                                                                                                                                                                                                                                                      1167 CATAACGTCACAGAGAGTTCAAGAGTTACAACAAGCACGCATTTGCAACTCTGTCCTTC 1226
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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ilarity 46.2%; Pred. No. 0.0069;
Conservative 0; Mismatches 171;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/255,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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US-09-815-242-7730
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Matches 147; Conserv
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US-09-815-242-7730
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786 GCTCGGGCCGCGCTCGGTGTTCGCCCATGGCGTGCACCTGTGCGACGGCGAATGCCAGCG 845
                                                                                                                 846 CCTGGCGGAGACTGGCTCGGCGGTGGCGTTCTGCCCGACCTCCAACCTGTTCCTCGGCAG 905
                                                                                                                                                                       479 CGCCGTGGTGATCTTGCTGATGACCAAAGGGAAGAGCTCGCACTTATTCGTCTTCAGTGA 538
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                                                     CCTCGAGGAGAATCGCTGGGTCAATGAGTCCATCACCGCGCTCATCATCGGGCTCTGCAC 478
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| Sequence 9, Application US/10033109
| Patent No. US20020142390A1
| GENERAL INFORMATION:
| APPLICANT: Allen, Stephen M. |
| APPLICANT: Rafalski, J. Antoni |
| APPLICANT: Rafalski, J. Antoni |
| APPLICANT: Rakal, Halime |
| TILLE OF INVENTION: Nitrogen Transport Metabolism |
| FILE REFERENCE: BB-1210 |
| CURRENT APPLICATION NUMBER: US/10/033,109 |
| CURRENT FILING DATE: 2001-12-28 |
| PRIOR PLLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/384,625 |
| PRIOR PLLING DATE: RARLIER PILING DATE: 1999-08-27 |
| PRIOR PLLING DATE: BARLIER PILING DATE: 28 August 1998 |
| NUMBER OF SEQ ID NOS: 14 |
| SOFTWARE: Microsoft Office 97 |
| SEQ ID NO 9 |
| LENGTH: 1883 |
| LENGTH: 1883 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1026 GCAGTTGCAGGGCGCCCG 1043
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US-10-033-109-9
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US-10-033-109-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 CGGTGGGTGGCCGGAGAAGTCGCCGCCGGTGAGGCATGGGGGATGGAGGTGGCGGCGCCGC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
APPLICANT: Budworth, P.
APPLICANT: Budworth, P.
APPLICANT: Chang, H.
APPLICANT: Chang, H.
APPLICANT: Han, T.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REPERENCE: 1360.001031
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.8%; Score 43; DB 10; Length 690; Best Local Similarity 49.3%; Pred. No. 0.012; Matches 112; Conservative 0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MCCOY, John
LaVallie, Edward
Radallie, Edward
Merberg, David
Tracy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
NUMBER OF SEQUENCES: 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 ATGAGTCCATCACCGCGCTCATCATCGGGCTCTGCACCGGCGTGGTG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                            CUKKENT FILING DATE: 201-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR APPLICATION NUMBER: US 60/259,692
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/259,692
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 816
LENGTH: 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 929, Application US/10040739 Patent No. US20020173635A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: U.S.A
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US-09-887-576-816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-040-739-929
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Search completed: April 5, 2003, 17:54:07 Job time: 223 secs

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BQ316128
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BM10459
BM10451
BM660526
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	Description	AY105332 Zea mays	AY109416 Zea mays	AU094795 AU094795	BJ312595 BJ312595	BE420587 HWM000.D1	BQ865196 QGC2a03.y
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	Query re Match Length DB ID	2080	3272	711	719	1212	069
de	Query Match	35.5			24.3	20.3	17.7
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B1933988 B316128 B0512490 B06121460 B0612167 B0163913 B0163913 B019321 B01832 BM66097 BM66097 BM66097	BQ034865 A1938253 BE440835 A2110110 AL822495 AW685820 BQ508685 AV909979 BQ508685 AV408114 BW660527 BW660527 BW66527 BW66527 BW66527 BW746114 BW746114 BW746114 BW746114 BW746114 BW7499998 BW74999998	BE49875 BE49875 BE607274 BE607262 BE597324 BE597324	080 k equer Stre pogoi pogoi ont 211, ers 211, 4577			
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                                                          /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs, this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
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Oryza sativa (japonica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 711)
Sasaki, T. and Yamamoto, K.
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                Unpublished (2000)

Contact: Takuji Sasaki

National Institute of Agrobiological Resources

Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
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                                                                                                                       Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT ='RGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGTCACCTCTGAGCCTTCATCACCAAAGTCCCTGCATTCT-CCTCTCCTGACAAGCATG 1706
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                                                                                                                                                                         Location/Qualifiers
1. .711
/organism="Oryza sativa (japonica cultivar-group)
/cultivar="Nipponbare"
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                                                                                                                                                                                                                                                                                                                                                                                      Length 711;
                                                                                                                                                                                                                                            /db_xref="taxon:39947"
/clone="B31666"
/clone_lib="Rice panicle shorter than 3cm"
/dev_stage="shorter than 3cm"
/dev_stage="shorter than 3cm"
/dev_stage="norgan: panicle"
/159 c 172 g 187 t 1 others
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Pred. No. 3.8e-128;
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99.4%;
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/urganism="Triticum aestivum"
/cultivaz="Chinese Spring"
/db_xref="Lexon:4565"
/clone=lib="xy Ogihara unpublished cDNA library, Wh_yf"
/clone=lib="spikelet at early flowering"
/clone=lib="xy Ogihara unpublished cDNA library, Wh_yf"
/clone=lib="xy Colhara unpublished cDNA library, Wh_yf"
/clone=lib="xy Colhara unpublished cond flowering"
/dev. stage="Feekes" scale 6"
/dote="yector: Lambda Uni-ZAP XR, excised phagemid;
Site=1: ExoR1; Site=2: Xho!; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hydroponic conditions at UC Davis, salt stressed for 12
hydroponic conditions at UC Davis, slant excessed for 12
hydroponic conditions at UC Davis, as present for 12
hydroponic conditions at UC Davis, as present for 12
hydroponic conditions and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
/ Choi, Close, Fenton, Kianian, Otto, Simons, Zhang)
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
                                                    BJ312595 Y. Ogihara unpublished cDNA library, Wh_yf Triticum aestivum cDNA clone whyf10p07 5', mRNA sequence.
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Ogihara;Y. and Murai,K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Pred. No. 5e-109;
0; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                            BJ312595.1 GI:20119380
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ilarity 87.9%;
Conservative
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Best Local Similarity
Matches 617; Conserv
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RESULT 4
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Query Match
Best Local Similarity 73.04
Matches 651; Conservative
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HWW000.D12 ITEC HWM Barley Leaf Library Hordeum vulgare cDNA clone
אאר האוא sequence.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae
; Triticeae, Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Jodrier, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Rabburton, M. and Wenzel, G.
International Triticae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4513"
/clone="HWM000.D12"
/clone=lib="TIEC HWM Barley Leaf Library"
/tissue_type="leaf"
/dev_stage="14 day old"
/note="Vector: pBluescriptSK(-); 850 bp average insert
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                                                                                                                                                                                                                                                                               1349 TCTGATTGGAAGAGCTGCTTTTGTATTCCCGCTGTCGTTCTTGTCGAACCTAACAAAGAA 1408
                                                                                                                                                       1229 TGCTGAGACTTTTCTCTTCCTGTATGTTGGGATGGATGCATTGGATATTGAAAAATGGGA 1288
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258 TGAGGTCGCACTTGTGATGCTCATGGCCTACCTCTCATATATGCTAGCTGAGCTGCTAGA 317
                           378 TAACGTGACAGAGAGCTCAAGAGTTACAACAAAGCATGCGTTTGCAACCTTGTCCTTCAT
                                                                                                                                                                         438 TGCCGAGACTTTTCTCTTCCTTTATGTTGGGATGGATGCACTGGATATTGAGAAGTGGAA
                                                                                                                                                                                                                                                                                                558 TCTGGTTGGAAGAGCTGCTTTCGTCTTCCCGCTCTCGTTATCCAACCTGACAAGAA
                                                                                         1169 TAACGTCACAGAGAGTTCAAGAGTTACAAGAAGCACGCATTTGCAACTCTGTCCTTCAŢ
                                                                                                                                                                                                                                498 ATTIGCTAGTGACAGCCCTGGCAAATCCATIGGAATAAGCTCAATTTTGCTCGGATTGGT
                                                                                                                                                                                                                                                                                                                                            GGCACCGAATGAAAAATAACCTGGAGACAGCAAGTTGTAATATGGTGGGCTGGGCTGAT
                                                                                                                                                                                                                                                                                                                                                                          Contact: Herrmann RG
Botanisches Institut der LMU
Menzinger Str. 67, D-80638 Munchen GERMANY
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690 bp mRNA linear EST 14-AUG-2002
QGC2a03.yg.abl QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
QGC2a03, mRNA sequence.
BQ865196
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                                                                                                                    600 AAAAAGCAATTCTTCCGGAATTTCATGACGATCACATTATTTGGAGCCGTCGGGACAATG
                                                                                                                                                        57 AGAGAACAATTCTTCCGCAATTTCATGACTATTACATTGTTTGCCGTAGTTGGGACCTTG
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                                                                                                                                                                                                                                                                                                                                                            720 ACGCTGGATGTAGGAGATTTTCTTGCAATTGGAGCCATCTTTTCTGCGACAGATTCTGTC
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   Length 1212;
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20.3%; Score 473.2; DB 10; Length
73.0%; Pred. No. 1.5e-89;
tive 0; Mismatches 233; Indels
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TTTGCTGGATTGCTCAGTGCATACATAATCAAGAAGCTATACATTGGAAGGCATTCTACT 1043
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/clone lib="tomato flower,
/tissue_type="flower"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGTTCTGATTGGAAGAGCTGCTTTTGTA 1373
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/db_xref="taxon:ds"
/dlone="voc2ad3"
/clone="voc2ad3"
/lab host="voc2ad3"
/lab host="voc2ad3"
/lab host="voc1a"
/lab host="voc1a"
/lab host="wector: pBRcDNA&fiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_IIB=_GABCDI lettuce salinas
TAG_IIS=_GABCDI lettuce salinas
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Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
                                                                Lactuca sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids II, Asterales, Asteraceae, Lactuceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 1.(530)-742-1742

Fax: 1-(530)-752-9659

Famil: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]

belongs to contig QG_CA_Contig6585, see http://cgpdb.ucdavis.edu/

for details.
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); Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
University of California at Davis (UCD)
Amandson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'organism="Lactuca sativa"
'cultivar="Salinas"
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GI:22250661
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                                               Lactuca sativa.
  BQ865196.1
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B1933988 665 bp mRNA linear EST 18-OCT-2001
EST553877 tomato_flower, anthesis Lycopersicon esculentum cDNA
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
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/note="Vector: pBluescript SK(-); Site_1: BcoRI; Site_2:
Xho1; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
140 c 144 g 225 t
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van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,
Ulterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fraser, C.M.,
Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, anthesis (2001)
Unpublished (2001)
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Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
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                                                                           TITGITGCTGAGTTATTTATCTTTATGTCGGAATGGATGCTTTAGATATTGAAAAG
301 GGAGCTGGGCTACTAAGTGCTTATATATAAGAAGCTATATTTTGGAAGGCATTCAACT
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/cultivar="TA496"
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1 (bases 1 to 632)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Umpublished (2002)
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                           Length 665;
                          Score 400.6; DB 13; Length
Pred. No. 3.5e-74;
0; Mismatches 164; Indels
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                           17.2%;
75.3%;
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Triticum aestivum
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
TT: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Triticum aestivum"
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Location/Qualifiers
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QGGSE06.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone BU0004460
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van bamme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project
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Mararyota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, euasterids II, Asterales, Asteraceae, Lactuceae,
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Asmundson Hall UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Fax: 1-(550)-752-9659
Fax: contig OG_CA_Contig6585, see http://cgpdb.ucdavis.edu/for details.
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Unpublished (2002)
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(bases 1 to 802)

(bases 1 to 802)

Reall, C.K., Hart, A., Baker, B., Tankaley, S., Fry, W., Smart, C., Restrepo, S., Giiffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A.
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Other ESTS: EST619906
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9/12 Medical Center Dr. Rockville, MD 20850, USA

Email: potato@tigr.org

This clone is available through the Research Genetics, conta

Research Genetics for further information 1-800-711-6195 or
Seq primer: T3.
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Pred. No. 5.2e-72;
0; Mismatches 233; Indels

    802
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjte"

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                                                                                               /noce="Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. CDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize
                                                                                                                                                                                                                                            size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB=QG_EFGHJ lettuce serriola
TAG_LISSUB=flowers environmental stress
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                                                          'clone_lib="QG_EFGHJ lettuce serriola"
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cultivar="L.serriola"
                 /db_xref="taxon:4236"
/clone="QGG5E06"
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ECORI adapters (5'0H-AATTCGGCAGAG and 3'GCGGTGTCTC) were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction sites of the pBluescript vector. The vector was previously dephosphorylated. The ligated cDNA fragments were transformed into DH10B by electroporation. Library is in LB medium with ampicillin and glycerol as Average insert size: 800 bp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                 Sap8dd01.y1 Gm-c1087 Glycine max cDNA linear EST 26-jUN-2002 sap8dd01.y1 Gm-c1087 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1087-7057 5' similar to TR:Q9SS27 Q9SS27 PUTATIVE SODIUM PROFON EXCHANGER. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                    Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Mylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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/clone="SOYBEAN CLONE ID: Gm-c1087-7057"
/clone lib="Gm-c1087"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shoemaker R/Public Soybean EST Project
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High quality sequence stop: 479.
Location/Qualifiers
                                                                                                                                           BQ612167
BQ612167.1 GI:21601836
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                                                                                                                                                                                                                                         Glycine max
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                                                                   DEFINITION
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RESULT 11
BQ612167
LOCUS
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AUTHORS
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JOURNAL
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KEYWORDS
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638 bp mRNA linear EST 09-APR-2002
BJ317459 Y. Ogihara unpublished cDNA library, Wh_yf Triticum
aestivum cDNA clone whyf28e02 5', mRNA sequence.
BJ317459 GI:20122274
EST.
library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synchesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digeated pUG19 vector. Blue/white selection on carbenicillin-containing plates was used to recover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTGCTGGATTGCTCAGTGCATACATAATCAAGAAGCTATACATTGGAAGGCATTCTACT 1043
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Pred. No. 7.8e-66;
0; Mismatches 190;
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Best Local Similarity 71.4%;
Matches 475; Conservative
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952081B08.x1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
clade, Panicoideae, Andropogoneae, Zea.
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  85 ATCAGTGGTGCTTTTCAATGCAATCCAAAGCTTTGACCTCAACCAAATTGACTCTTCAAT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="suspension culture"
/dev_stage="mixed logarithmic and stationary growth
phases"
                                                                                                                                                                                                                                                                                                                                ATGTTATCTGAGTGGCATTCTCACTGTATTCTTTTGTGGTATTGTTATACT
                                                                                                                                                                         1103 GCTAGATTTGAGCGGCATTCTCACCGTATTCTTCTGTGGTATTGTAATGTCACATTACAC
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                                                                                                                                                                                                                    1043 IGACCGIGAGGIIGCCCTIAIGAIGCICAIGGCTIACCTITICAIAIAIGCIGGCTGAGTI
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/organism="Zea mays"
/oultivar="BMS (Black Mexican Sweet)"
/db.xref="taxon:4577"
/clone_lib="952 - BMS tissue from Walbot
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Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: walbot@stanford.edu
Plate: 952081 row: B column:
Location/Qualifiers
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="Y. Ogihara unpublished cDNA library, Wh_yf"
/tissue_type="spikelet at early flowering"
/tissue_type="spikelet at early flowering"
/dev stage="Feekes" scale 6"
/note="voctor: Lambda Uni-ZaP R, excised phagemid;
Site 1: ECORI; Site 2: Khol; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGAGGAGAATCGCTGGGTCAATGAGTCCATCACCGCGCTCATCGTCGGGCTCTGCACG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 TICCCCGGAAICTITCICICTCTGACGAGGAGCAGGCGGCGGCGGGAIGGGGIACCAAG 173
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                                                                                     Triticeae; Triticum.

(Dases 1 to 638)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 15.4%; Score 359.4; DB 1 Best Local Similarity 75.9%; Pred. No. 1.7e-65; Matches 444; Conservative 0; Mismatches 141
                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whyf28e02"
                                                                                                                                                                                                                                                                                                                                                   Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                          Triticum aestivum
bread wheat
                        ORGANISM
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: Khol; supplier: Cornell University, Tankaleylab.
sequencing; The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium.

cuttings from in vitro grown plants on medium."
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

(bases i to 637)

van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S., Vtreback,T., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.,

Tanksley,S. and Baker,B.

Generation of ESTs from potato roots

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1084 CATATATGCTGGCTGAGTTGCTAGATTTGAGCGGCATTCTCACCGTATTCTTGTGGTA 1143
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                                                                                                                                        720
                                                                                                                                                                                                              534 TGTCGTTTTTCACAATATCTCTTGCTGCCATTGCGAIATTCAGCAGGATGAACATTGGGA 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 ACGCTTTGCAACTTTGTCATTTCTTGCAAAGATTTCCTCTTTCCTCTATGTCGGCATGG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cdna@resgen.com
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
601 AAAAGCAATTCTTCCGGAATTTCATGACGATCACATTATTTGGAGCCGTCGGGACAATGA
                                               474 AGAAGCAGTTCTTCCGGAATTTCATGACAATCACATTTTGGTGCCGTTGGACGATGA
                                                                                                                                        661 TATCCTTTTTCACAATATCTATTGCTGCCATTGCAATATTCAGCAGAATGAACATTGGAA
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/clone lib="potato roots"
/tisue_type="roots"
/dev stage="in vitro grown stem cuttings"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                            Contact: Research Genetics, Libraries Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Solanum tuberosum"
/cultivar="Kennebec"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4113"
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Email: cdna@resgen.e
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                 1383
1264 ATGCATTGGATATTGAAAAATGGGAGTTTGCCAGTGACAGACCTGGCAAATCCATTGGGA 1323
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National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
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                                                                                                                                                                                                                                                                                                                                                302 CATTCTTCTCCCAACTTAATGAAGAAATCCTCGGAGCAAAAAATTACCTTTAGGCAGGAAG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 Igaraarardigegegegerridardadadegegeacrereceregeacrerarara 421
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                                          1324 TAAGCTCAATTTTGCTAGGATTGGTTCTGATTGGAAGAGCTGCTTTTGTATTCCCGCTGT
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Sasaki,T. and Yamamoto,K.
Rice cDNA from panicle
Unpublished (1997)
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1013 CAAGAAGCTATACATTGGAAGGCATTCTACTGACCGTGAGGTTGCCCTTATGATGCTCAT 1072

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1 CAAGAAGCTATACATTGGAAGGCATTCTACTGACCGTGAGGTTGCCCTTATGATGCTCAT 60
                                       GGCTTACCTTTCATATATGCTGGCTGAGTTGCTAGATTTGAGCGGCATTCTCACCGTATT
                                                                                                                             CTTCTGTGGTATTGTAATGTCACATTACACTTGGCATAACGTCACAGAGAGTTCAAGAGT
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EST 04-APR-2002
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Oryza sativa (japonica cultivar-group)

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzae, Oryza.

I bases 1 to 378)

Saski, T. and Yamamoto, K.

Rice ODNA from panicle

Unpublished (1997)
1264 ATGCATTGGATATTGAAAATGGGAGTTTGCCAGTGACAGACCTGGCAAATCCATTGGGA 1323
                                                                                                                                                                          TIGIAATATGGTGGGCTGGGCTGATGAGGGGGCTGTGTCGATTGCTCTTGCTTACAATA 1503
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National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'
                           302 CATTCTTCTCCAACTTAATGAAGAATCCTCGGAGCAAAAATTACCTTTAGGCAGCAAG 361
                                                                                                                                                                                                                                                                                           482 TAACCATTGTTCTATTCAGCACAATGGTATTCGGTTTAATGACAAAACCCCTTATAAGTC 541
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C91832 Rice panicle shorter than 3cm Oryza sativa (japonica
cultivar-group) cDNA clone E31686_1A, mRNA sequence.
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                                                                                      TAAGCTCAATTTTGCTAGGATTGGTTCTGATTGGAAGAGCTGCTTTTGTATTCCCGGCTGT
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/dev_stage="shorter than 3cm"
/note="Organ: panicle"
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1013 CAAGAAGCTATACATTGGAAGGCATTCTACTGACCGTGAGGTTGCCCTTATGATGCTCAT 1072

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TACAACAAAGCACGCATTTGCAACTCTGTCCTTCATTGCTGAGACTTTTCTCTTCCTGTA 1252
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1 CAAGAAGCTATACATTGGAAGGCATTCTACTGACCGTGAGGTTGCCCTTATGATGCTCAT 60
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